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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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length: 100
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Match
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Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-08-669-721-1
US-09-189-344-1
US-09-189-344-1
US-09-189-344-1
S109931-4
US-08-145-705A-17
US-08-145-707A-3
US-08-985-162-813
US-08-985-162-813
US-08-985-162-813
US-08-985-162-813
US-08-985-162-813
US-08-985-162-813
US-08-985-162-814
US-08-261-28-819-39
US-08-680-506-18
US-08-680-506-18
US-09-288-461-20
US-08-368-819-37
US-08-368-819-37
US-08-468-819-37
US-08-468-819-37
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(without alignments)
78.173 Million cell updates/sec
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3, Appli
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467, App
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US-08-480-784-72	US-09-302-620B-8	US-09-258-408-98	US-09-258-408-97	US-08-594-452-98	US-08-594-452-97	US-07-722-798A-73	US-09-514-302-10	-561	US-07-722-798A-74	US-08-337-120A-33	US-09-144-112-24	US-09-196-132-25	408-	US-09-094-405-29	US-08-281-203-18	US-08-578-686C-24	US-08-594-452-25
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ALIGNMENTS

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RESULT 2
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LENGTH: 29
TYPE: DNA
                                                                                                                                                                                                 Sequence 1, Application US/08669721
Patent No. 5834236
GENERAL INFORMATION:
APPLICANT: Lamb et al., Christopher J.
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE T NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 112, Application US/09593012 Patent No. 6387652 GENERAL INFORMATION:
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APPLICANT: WESPER, Stephen
TITLE OF INVENTION: METHOD OF IDENTIFYING AND QUANTIFYING SPECIFIC FUNGI AND BACTE
FILE REFERENCE: HAUGLAND-1A
CURRENT APPLICATION NUMBER: US/09/593,012
CURRENT FILING DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 09/290,990
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR APPLICATION NUMBER: US 60/081,773
PRIOR APPLICATION NUMBER: US 60/081,773
NUMBER OF SEQ ID NOS: 225
NUMBER OF SEQ ID NOS: 225
CTATE: CA
COUNTRY: USA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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                                                                                                    STREET: 422.
STREET: 422.
CITY: La Jolla
STATE: CA
TISA
                                                                                                                                                                ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
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Local Similarity 76.9%;
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                                   Floppy disk
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Pred. No. 1.6e+03;
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US-08-669-721-1/c
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Query Match
Best Local Similarity
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APPLICANT: Lamb e
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                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLODS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/669,721
FILING DATE: 27-UN-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Ellison, Eldora L.
REGISTRATION NUMBER: 39,967
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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REGISTRATION NUMBER: 39,967
REFERENCE, DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
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NAME: Ellison, Eldora L.
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CTTY: La Jolla
                                                                              LENGTH: 36 base pairs TYPE: nucleic acid STRANDEDNESS: single
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CLASSIFICATION: 435
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OPERATING SYSTEM:
SOFTWARE: Patentl
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619/678-5099
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619/678-5099
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VENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND

VENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
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linear
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76.9%;
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PC-DOS/MS-DOS
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1.6e+03;
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                                                                                                                                                         Sequence 1, Application US/09189344 Patent No. 6191258
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                                                                                                                                                                                                                                                                                                                        Matches 10;
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Lamb e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                           ADDRESSEE: Fish & R.
                                                                           APPLICANT: Lamb et al., Christopher J.
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NO TITLE OF INVENTION: TR NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ellison, Eldora
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
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La Jolla
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                              4225 Executive Square, Suite 1400
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VENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
VENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                          Conservative
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                                             Fish & Richardson P.C
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76.9%;
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Pred. No.
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RESULT 6
5190931-4
WESULT 7
US-08.145-705A-17/c
US-08.145-705A-17/c
Sequence 17, Application US/08145705A
Patent No. 5489513
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TITLE OF INVENTION: REGULATION OF GENE EXPRESSION BY
EMPLOYING TRANSLATIONAL INHIBITION OF MRNA UTILIZING
INTERFERINF COMPLEMENTARY MRNA
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Patent No. 5190931
                                                                                                                                                                                                                                                                                       SEQ ID NO:4:
                                                                                                                                                                              Matches
                                                                                                                                                                                             Query Match
Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/669,721
APPLICATION UMBER: US 08/669,721
FILING DATE: 27-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ellison, Eldora L.
REGISTRATION NUMBER: 39,967
REGISTRATION NUMBER: 07251/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/(FILING DATE: 15-NOV-1989)
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                         42 AATCAATAACTTA 54
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 300,741
FILING DATE: 23-JAN-1989
APPLICATION NUMBER: 228,852
FILING DATE: 03-AUG-1988
APPLICATION NUMBER: 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 543, FILING DATE: 20-OCT-1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      LENGTH: 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AATCAANNANTTA 13
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nl Similarity 76.9%;
10; Conservation
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76.9%;
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                                                                                                                                                                            Score 10; DB 6; Length 96; Pred. No. 1.5e+03; 0; Mismatches 3; Indels
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Pred. No. 1.6e+03;
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GENERAL INFORMATION:

APPLICANT: Springer, Wolfgang; race;

APPLICANT: L bberding, Antonius

TITLE OF INVENTION: SPECIFIC GENE PROBES AND

TOP OF INVENTION: PROCESSES FOR THE DIAGNOSTIC

TOP INVENTION: INVESTIGATION OF CANDIDA
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US-07-737-071A-3/c
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                                                                                                                                                                                                                   sequence 3, Application US/07737071A
Patent No. 5229286
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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SOFTWARE: WORDERFIECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,705A
FILING DATE: October 28, 1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UMBER: German P 42 36 708.5
FILING DATE: October 30, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                         GENERAL INFORMATION: JARSCH, Michael
APPLICANT: JARSCH, Michael
APPLICANT: LANG, Gunter
TITLE OF INVENTION: CLONING AND OVEREXPRESSION OF
TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGENASE FROM LEUCONOSTOC
TITLE OF INVENTION: DEXTRANICUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: BarTELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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   STREET:
                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                     56 AATCAATAAATTA 44
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                            10;
SEE: Murray: 1725 K Street, N.W., Suite 1000 Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SPRUNG HORN KRAMER & WOODS 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida albicans
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                                                       Armstrong, Nikaido, Marmelstein Kubovcik &
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76.9%;
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Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 100;
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COMPUTER READABLE FORM:

COUNTRY:

United States of America

20006

MEDIUM TYPE:

Floppy disk

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JARSCH, Michael

APPLICANT: LANG, Gunter

TITLE OF INVENTION: CLONING AND OVEREXPRESSION OF

TITLE OF INVENTION: GLUCOSE-6-PHOSPHATE DEHYDROGEN

TITLE OF INVENTION: DEXTRANICUS
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 24 158.
FILING DATE: 30-JUL-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 22,890
REFERENCE/DOCKET NUMBER: 911028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
                                                                                                                                                                           CURRENT APPLICATION DATA:
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FILING DATE: 30-JUL-1990
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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TELEFAX: 440142
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
APPLICATION NUMBER: US 07/737,071 FILING DATE: 30-JUL-1991
                                                                                                                                   APPLICATION NUMBER: UPFILING DATE: 19930225
                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AAYCAATTATTTM 39
                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Murray, Robert B. REGISTRATION NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 19910
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 70.8%;
Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                  D.C.
                                                                                                                                                                                                                                                                                                                                                                    E: Nikaido, Marmelstein, Murray & Oram 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 887-0357
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                                                                                                                                                       US/08/022,096
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Pred. No. 4.4e+03;
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US-08-334-847-467
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                         TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      SOFTWARE: WOR'D PERFECT 5.1.
CURRENT APPLICATION DATA:
APPLICATION NUMBERS
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                  TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/334,847
FILING DATE: NO. 5693532ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION
TITLE OF INVENTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AAYCAATTATTTM 39
                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 72 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Chin, Monica F. REGISTRATION NUMBER:
                 FOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AATCAANNANTTA 13
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3. 5693532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McSwiggen
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               linear
                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHOD AND REAGENT FOR INHIBITING RESPIRATORY
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Query Match

69.28;

Score 9;

DB 1;

Length 15;

Best Local Similarity 50.0 Matches 6; Conservative

50.0%;

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Pred. No. 5.9e+03; 3; Mismatches 3;

Indels

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Gaps

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RESULT 12
US-08-985-162-813/c
; Sequence 813, Application US/08985162
; Patent No. 6057156
; Patent No. 6057156
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US-08-985-162-812/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 812,
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/985,16
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: IBM P.C. DOS 5.1
SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                16 AATCAAATACTT
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                                                                                                                                                              1 AATCAANNANTT 12
                                                                                                                                                                                                                Local
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                                                                                                                                                                                               Similarity 9; Conserv
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633 West Fifth Street
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McSwiggen, James
VENTION: ENZYMATIC NUCLEIC ACID TREATMENT
                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04 December 1997
N: 514
                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                              69.2%;
75.0%;
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                                                                                                                                                                                               0,
                                                                                                                                                                                               Score 9; DB 3
Pred. No. 5.9e
0; Mismatches
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5.9e+i
                                                                                                                                                                                                                .9e+03
                                                                                                                                                                                                                            Length 17;
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US-08-985-162-814/c
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 813:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 814, Application US/08985162 Patent No. 6057156 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5" Diskette, 1.44 MEDLUM TYPE: Storage
COMPUTER: IHM COMPATIBLE COMPUTER: IHM COMPATIBLE COMPUTER: IHM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                APPLICANT: McSwiggen, James TITLE OF INVENTION: ENZYMAT TITLE OF INVENTION: OF DISE
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                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Akhtar, Saghir APPLICANT: Fell, Patricia
                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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STATE: California
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TOPOLOGY: linear
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                                                                        ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 AATCAAATACTT 3
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                                          Los Angeles
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California
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633 West Fifth Street
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VENTION: ENZYMATIC NUCLEIC ACID TREATMENT
VENTION: OF DISEASES OR CONDITIONS RELATED
VENTION: TO LEVELS OF EPIDERMAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A
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Pred. No.
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Gaps

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RESULT 14
US-09-241-581B-2
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TOPOLOGY:
US-08-985-162-814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09241581B
Patent NO. 6350859

GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
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SOFTWARE: FBSTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY_AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELEFAX: (404) 873-8
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
FORMATTON: 67-3510
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US-09/241,581B
FILING DATE: 02-Feb-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
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Local Similarity 75.0%;
les 9; Conservative
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                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: Georgia
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; Sequence 2, Application US/08265428
; Patent No. 649289
; GENERAL INFORMATION:
APPLICANT: Krieger, Monty
TITLE OF INVENTION: Class BI Scav.
NUMBER OF SEQUENCE: 6
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 18 SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-241-5818-2
                                                                                                                                                                                                                                                  TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 2:
                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO ANTI-SENSE: NO PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 30309-4530
COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION UNMBER: 31,284
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                JOURNAL: J.
                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 |
CITY: Atlanta
                               PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
RELEVANT RESIDUES IN SEQ ID
                                                           AUTHORS: Ashkenas, et al. JOURNAL: J. Lipid Res.
                                                                                                                                                                                                                     LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
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AUTHORS: Ashkenas, et
JOURNAL: J. Lipid Res.
VOLUME: 34
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VOLUME: 983-1000
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STRANDEDNESS: single
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DATE: 1993
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1100 Peachtree Street,
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 PANR LOCUS DEFINITION		44 45		44	ω			υw	u u	c 31		งผ	N N	c 24	NN	21	c 19	17 18	15 16	سو مبو	c 12			0 7		-))	Result	
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control element. subdivision; Pseudomonadaceae; rmann, Institut f Mikrobiologie ETH	DNA linear BCT 18-NOV-1997		മറ	AL133423 Streptomy AC098321 Rattus no	AL392175 Streptomy AL161755 Streptomy	AE012548 Xanthomon	Strepto	NOV	04866 Novel	iomo s		Novel	Rattus	APOO4267 Oryza sat AL391763 Streptomy	Oryza sa	n on	AP003928 Oryza sat AP004683 Oryza sat	Oryza sa	Streptom	duman F	Homo sap	AF033262 Pseudomon	3 G		-	aerug	X97981 P.aeruginos	7736 P.a 8276 Pse	Description	

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Submitted (25-FEB-1992)
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Anaerobic growth and cyanide synthesis of
depend on anr, a regulatory gene homologou
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revised by [3]
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CGGCCTTGGCGTCCGCGGCGCGCGCGCGATGAGGGCGGCACCTGGGTGGTGATCCAGCCAC
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Bacteria; Proteobacteria;
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/strain="PAO1"
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/db_xref="GI:151025"
/translation="MT"
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FVQRYIEADFSHIGAMDARGFLIGSAVAYALNKPLVLFRKQGKLPADVLAEGYQTEYG
EAFLEVHADSLCEGDSVLIFDDLIATGGTLLAAASLVRRLGARVFEAAAIIDLPELGG
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/protein_id="AAA25714.1"
/db_xref="GI:151024"
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Submitted (16-MAY-2000) Department of Medicine and Genetics, Submitted (16-M
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Stover,C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentho, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, M.Y.
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/translation-"MNPPLPHERYHPEPLASGSIEASATTCQCCGKARGYVYTGSPYS
RHELPPGSLCPWCIADGSAAARYEASFSDDYPLLDAGVAADIVTEVCERTPGYTSWQQ
ERWLVCCEDACAFRGDAGREEIGQLGAEGLAQRFADFAWPAITWQRLVDAYTPGGNPA
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QALTAAMEGVCHCRQCRTLSEELCPQCADPRRDDSLLCVVEGPLDVFAVEQTGYRGR
YFVLKGHLSPLDGLOPEAIGIPELEARIRDGARSEVILATNPTVEGEATAHYIAQLLA
GRGLTLSRIAHGVPLGGELELVDGGTLAHALAGRRPIS"
                                                                                                                                                                                                                                                                                                                                                                   complement(1950. .2489)
/gene="PA1536"
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ITSGVRADYYTVAVRTGGEGFAGISLLLVEKGTAGFSVGRKLKKMGWWASDTAELFFD
DCRVPAENLIGVENAGFACIMANFQSERLALAVMANWTAQLALEESLRWAREREAFGK
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789. .1937
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                                                                                                       /product="conserved hypothetical protein"
/protein_id="AAG04925.1"
/db_xref="GI:9947495"
                                                                                                                                                                                                                                                                                                                                 complement(1950.
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YLKAGAAGILGIGYPEAYGGSCEGDLFAKVAASEELMRCGSGGLVAGLGSLDIGLPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="probable acyl-CoA dehydrogenase"
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/strain="PAO1"
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/transl_table=11
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EAGLNPNTFYRHERDIDDLGLTMIRDISTQLRQPLRQLRREAATRAAPGARAQTTPFG
LDLERGRRYCRETYRLFFDFVBSNPAAFINGVBELHGASPVLRGALRQLMDEFAEDMS
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GAAVLQMMGVSLDAEASGQLEQAHAGQQQQQAEPAAPGQALAEQRPAHGDGGEDAEAA
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RAYLEKCWEKY KLØEKTLLNTELGKLAMDERQSLWHLHDAQGHNYTANAVVSGWGGLS
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VTANGLYDGNGREREFUDALIFCTGFTANDPIPRGVYPGRDGRDLLDSWSKGPBAYKGT
TTAGFPNLFFLMGPNTGLGHNSMYYMLESQIAYVLDALKLMKRRELLSLEVKAPVQER
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TPLAALSNEARQQAEGVPA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical protein"
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/protein_id="AAG04927.1"
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 GCGTCGCGAACTTGAGCCCCCTTTTCGTCGCCCCTTGACAGGGTGCGACAGGTAGTCGCA
                                      TGAGGGTCAACATTCCAGTCACTCCGGGAAAAATGGAATTCTTCCATTGGATCGGCCCAC
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complement(6946. .7782)
/gene="PA1542"
complement(6946. .7782)
/gene="PA1542"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                /product="transcriptional regulator Anr"
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ADERIATFLYNLSARFFARGFSAQQFFILAMSRNEIGNYLGLAVETVSRVFTRFQONGL
ISAEGKEVHILDSIELCALAGGQLEG"
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/gene="anr"
/codon_start=1
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EAFLEVHADSLCEGDSVLIFDDLIATGGTLLAAASLVRRLGARVFEAAAIIDLPELGG
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AUTHORS
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Fachbereich Biologie, Philipps-Universitaet Marburg,
Karl-von-Frisch-Str., D-35032 Marburg, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 2635)
Hungerer,C., Troup,B., Raemling,U. and Jahn,D.
Cloning and regulation of the Pseudomonas aeruginosa hemN gene
encoding an oxygen-independent coproporphyrinogen III dehydrogenase
Unpublished
2 (bases 1 to 2635)
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                                                                                                                                          /product="oxygen-independent coproporphyrinogen III

dehyrogenase"
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/db_xref="GI:1513308"
/db_xref="SWISS-PROT:P77915"
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GLLREIGFRRYSLGVQDEDMEYQRAVNLRWQTPEETRTIVBARTLQYRSINLDLIYGL
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GLLREIGFARRYSLGVQDEDMEYQRAVNLRWQTPEBERMPQRRINADDLSPGGKLEMLGAR
GLLREIGFARRYSLGVQDEDMEYQRAVHLPBERMPQRRINADDLSPGGKLEMLGR
GIGDLYSQNSSDINDYQTSLDNGQLAIRGLHGNSDDKYRRAVIQQLIGHFELAFEDI
QIGDLYSQNSSDINDYQTSLDNGQLAIRGLHGNSDDKYRRAVIQQLIGHFELAFEDI
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709. .:
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632. .645
                                                                                           complement(2140.
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                                                                                                                            ETEFGIDFRSYFAELWPDLERFAADGLIRPDAKGIDITSSGRLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="hemN"
709. .2091
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/EC_number="1.3.3.3"
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/strain="PAO1"
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                                                         /codon_start=1
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                                                                                                                                                                                                                                                                     Identification and molecular characterization of a transcriptional regulator from Pseudomonas aeruginosa PAOI exhibiting structural and functional similarity to the FNR protein of Escherichia colimaterian (b), 1469-1481 (1991)
                                                                                                                                                                                               transcriptional activator of anaerobic gene expression which shows a high degree of amino acid similarity to FNR protein of E.coli. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Sawers, R.G
                                                                                                                                                                                                                                                                                                                                                                                                     Sawers, R.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
Pseudomonas aeruginosa
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X58405
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                                                                                                                                                                                                                                                                                                                                                                      Submitted (11-MAR-1991)
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                                                                                                 /gene="anr"
66. .>831
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971 c 779 g 463 t 1 others
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97. .831
                                                                                                                             /db_xref="taxon:287"
66. .831
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/trans_table=11
/product="transcriptional activator
/protein_id="CAA41305.1"
                                                                                                                                                       /organism="Pseudomonas
/strain="PAO1"
                                                         /gene="anr"
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Pred. No. 5.6e-38;
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Maria
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                                                                                                                                                                      aeruginosa
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Oryza sativa
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Oryza sativa (japonica cultivar-group).
Dryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                              Chromosome 10
On Mar 2, 200
                                                                                                                                                                                                                    Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873
                                                                                                                                                                                                                                                                                                                                                Submitted (08-JAN-2001) The Plant Genome Initiative at Rutgers Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873
                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 129420)
Llaca, V., Young, S., Kavchok, S.,
Nevill-Manning, C. and Messing, J.
                                                                                                                                                                                                                                                                         Direct Submission
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Llaca, V., Young, S., Ka
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HTG.
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TYPVSAQALETTSVCEIPFERLDELSBQLPQLRRQLMRLMSREIRDDQQMMLLLSKKT
ADERIATFLVNLSARFBRARGESAQOFRLAMSRNEIGNYLGLAVETVSRVFTREQQNGL
ISAEGKEVHILDSIELCALAGGQLEG"
261 g 164 t
                                                                                                                                                                2001 this sequence version replaced Location/Qualifiers
1. .129420
                                                                                                       /organism="Oryza sativa
/sub_species="japonica"
/db_xref="taxon:39947"
/chromosome="10"
                                                                         /clone="nbeb0040I11"
28213 c 30048 g
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Score 51.8; DI Pred. No. 10; O; Mismatches
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   Query Match
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Matches 113; Conserv
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                                                                                                                                                                                                                                                        Submitted (30-MAY-2002) The Plant Genome Initiative at Rutgers Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873, USA On May 30, 2002 this sequence version replaced gi:13184872. This BAC overlaps with rice BAC nbeb004011 (AC087547) and
                                                                                                                                                                                                                                                                                                                                                    4 (bases 1 to 141041)
Llaca, V., Song, R., Young, S., Kavchok, S., Ward, K. and Messing, J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-MAR-2001) The Plant Genome Initiative at Rutgers Waksman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08873
Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (bases 1 to 14104 Llaca, V., Young, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (08-JAN-2001) The Plant Genome Initiative at Rutgers Waksman Institute, Rutgers University, 190 Frelinghuysen Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 141041)
Llaca, V., Young, S., Kavchok, S., Clark, T., Charydczac, G., Linton, E.,
Nevill-Manning, C. and Messing, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Llaca, V., Song, R., Young, S., Kavchok, S., Ward, K. and Messing, J
Oryza sativa (japónica cultivar-group) chromosome 10 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Piscataway, NJ 08873
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                                                                                    /clone="nbeb0016G17"
31534 c 32795 g
                                                                                                                                        /organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                         /chromosome="10"
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                  10.5%;
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Score 51.8; DE Pred. No. 9.8; 0; Mismatches
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CCCGCGAAGCTCCGACACCACCCGCCGCCTCCTTCACCGCCGCCTCGTCGTCCGACAA 85886

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    N
                                                                                                                                                                                                                                                                                  AL Submitted (20-UN-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL.http://rgp.dna.affrc.go.jp/, Tel:81-998-38-7441, Fax:81-298-38-7468).

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced * by the finished sequence as soon as it is the accession number will be preserved.
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CTCGCGGATCATCTTCACCATCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCCGGCGGGTCTTCCGCCTGCTCGGCGGTGCCGGTCCGTGCGGCCTTGGCCGTC 193
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                                          al Similarity
105; Conser
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2 (bases 1 to 175644)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA,
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Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA clone:P0622F03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group) chromosome 6 *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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/cultivar="Nipponbare"
                                                                                                                                     /clone="P0622F03"
41378 c 40541
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/chromosome="6"
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53.3%;
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                                      Score 49.8; I
Pred. No. 21;
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                                                                          Length 175644;
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     Local Similarity 57.4 hes 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE2; HTGS_DRAFT.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadaceae; Chlamydomonas.
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Chlamydomonas reinhardtii clone
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The University Of Oklahoma
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On Jul 14, 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-JUL-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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                                                                                                                                                                                               the accession number will be preserved.

1 3364: contig of 13364 bp in length
13365 13464: gap of unknown length
13465 32124: contig of 18660 bp in length
32125 3224: gap of unknown length
32125 68736: contig of 36512 bp in length.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                          by the finished sequence as soon as it is available and
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/organism-"Chlamydomonas
/db_xref-"taxon:3055"
/clone-"cr-32m22"
                                                                                      /clone_lib="cr-32m22"
23005 c 23233 g 1
                  10.0%;
Score 49.4; D
Pred. No. 28;
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On Aug 3, 2002 this sequence version replaced g1:21747478.
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Direct Submission
Submitted (04-AUG-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
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Jia, H., Lin, S., Wu, H.,
Direct Submission
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3 (bases 1 to 102657)
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                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are presented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                 /organism="Chlamydomonas
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/clone="cr-3h1"
                                                                                                                                                                                         Location/Qualifiers
1. .102657
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32817 c 34503 g
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Score 49.4; Di
Pred. No. 26;
O; Mismatches
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AF061246
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Analysis of 4-phosphopantetheinylation of polyhydroxybutyrate
synthase from Ralstonia eutropha: generation of beta-alanine
auxotrophic Tn5 mutants and cloning of the panD gene region
J. Bacteriol. 181 (5), 1429-1435 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-APR-1998) Biology, Muenster, NRW 48149, Germany
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ppensack, A., Steinbuechel, A. and Rehm, B.H.A.
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                                                                                                        2169. .2531
/gene="panD"
                                                                                                                                                                                                                                                         /pseudo
991. .2
                                                                                                                                                                                                                                                                                                      /product="MutT" 991. .2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eutropha.
                                                                                                                                                         /product="NAD(P) transhydrogenase 2169. .2531
                                                                                                                                                                                                                                                                                                                                                                                                 complement(204. .704)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(204. .704)
/gene="mutT"
ELYNVNNGERFSTYIIKGERGSGEISLNGAAARRAHLGDQLIICTYAPMSDEEIAAYK
                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Ralstonia eutropha"
/strain="H16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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             translation="MQRIMLRAKLHRVTVTQADLNYEGSCGIDQDLLDAADMKEFEKI/
                                                                                            /codon_start=1
                                                                                                                                                                                                                       /pseudo
                                                                                                                                                                                                                                    /gene="pntAA"
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                                                                                                                                                                                                        'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 GATATCCTCGTCCTCCTCCACCGGCACCCCCATGGTAGCGGCCAGCTCGCCCCTGC 100
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AF033262
AF033262.1
                                                                                                                                                                                                                                                                                                                                   Submitted (06-NOV-1997) Biotechnology, Yonsei University, Soedaemun-Gu Shinchon-Dong 134, Seoul 120-749, Korea
                                                                                                                                                                                                                                                                                                                                                                        Her,S., Lee,H.-S. and Oh,D.-H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning and sequencing of beta-1,4-endoglucanase Pseudomonas sp. YD-15
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Pseudomonas sp. YD-15
Bacteria; Proteobacteria.
1 (bases 1 to 2450)
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Location/Qualifiers
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/codon_start=1
/transl_table=11
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a 1099 c 1063
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/product="endoglucanase"
/product="endoglucanase"
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TYARAAGHLGVAPNQGDTSVGAGSSCGYSLDVRGGWYDAGDHGKYVVNGGIATWQLQN
TYERTLHVAGADRAALGDGKAALPERGMVDPVLDEARWEVEELLRMQVPAGFTDAGN
VHHKMHDENWTGIFTIDDPQORRILAPVSTANTLNMAAVAAQASPVGAVDAGFAAGPL
SAARTAYAAAKANPNRLASDADGTGGGYGDPSVTDEFYWAAAELFATTGEAGYRADVT
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2771. :
                                                                                                                                                                                                      /note="carboxymethylcellulase; CMCase; member of
cellulase family 9"
                                                                                                                                                                                                                                                                        /strain="YD-15"
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                                                                                                                                                                                                                                                       /db_xref="taxon:72609"
                                                                                                                                                                                                                                                                                        ∕organism="Pseudomonas
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Direct Submission
Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology, Uniformed Submitted (02-MAR-2001) Biochemistry & Molecular Biology & Mole
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Homo sapiens BTBD2 protein mRNA,
AF355797 GI:13430407
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 3 (1), 1 (2002)
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                                                                          IREVRLENAVVRWSEAECQRQQLQVTPENRRKYLGKALGLIRFPLMTIEEFAAGPAQS
GILVDREVVSLELHFTVNPKPRVEFIDRPRCCLRGKECSINRFQQVESRWGYSGTSDR
IRFSVNKRIFVVGFGLYGSIHGPTDYQVNIQIIHTDSNTVLGQNDTGFSCDGSASTFR
                                                                                                                                             /translation="maaggsggrascppgygygpgtggspgpsaaaaatpapgnaaaa
Aaaaaaaaapgptppappgggtdaqaagababeaagpgaaalqpabaynwqaskpt
YQBEPAPEFRUEVLCDYHFLYKGKISSORIPAHFFYLAVKSAYEDAMFNGGMATTSTE
IELPDYBPAAFLALLKFLYSDEYQIGPETYMTTLYTAKKYAVPALEAHCYBELKKNLK
ADNAFMLLTQARLFDBPQLASLCLENIDKNTADAITABGFTDIDTTLYAVLEBDTLG
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LNQSYITGYGENPVRNYHHFWAHQADASLPTAPPGSLAGGPNSSLQDPLAAAQLAAC
APQKCYYDHIEAYSVNEVAINWNSALWADSRRAADARA"
9 949 c 885 g 277 t
        NGTSVEDGQIPEVIFYT 932 c 820
                                                     VMFKEPVEVLPNVNYTACATLKGPDSHYGTKGLRKVTHESPTTGAKTCFTFCYAAGNN
                                                                                                                                                                                                                                                                                      /product="BTBD2 protein"
/protein_id="AAK25826.1"
/db_xref="GI:13430408"
                                                                                                                                                                                                                                                                                                                                                                                         /note="BTB-containing Kelch-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                   /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo.
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23 CGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCCATGGTAGC
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AC004678
AC004678.1 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-MAY-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. Cosmid R34094 overlaps cosmid R77216 to the left and F20063 to the right.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Christensen,M., Georgescu,A., Avila,J., Liu,S., Attix,C., Andreise,T., Trankheim,M., Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Montgomery,M., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S.
                                                                                                                                                                                                                                                                                                                                                                                        Additional chr 19 map and sequence information may http://www-bio.llnl.gov/bbrp/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence analysis of a 3.5 Mb contig in serine protease gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Montgomery, M., Carrano, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkhart-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., Stilwa
Phan,H., Velasco,N., Garnes,J., Danganan,L., Poundstone,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 38939)
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                /note-"DDS similarity to T50998 yb71g05.s1 Homo sapiens cDNA clone 76664 3' contains MER22 repetitive element; (123. .1); 96% identity."
                                                                                  19 as its only human chromosome complement(82, 204)
(123. .1);
83. .239
                                                                                                                        /note="Cosmid library constructed at LLNL from flow-sorted chromosomes from hybrid 5HLZ-B, which carries chromosome of any human chromosome."
                                                                                                                                                                                                                                /cell_line="5HL2-B"
                                                                                                                                                                                                                                                      /map="19p13.3 between CDC34 and D19S342"
/clone="R34094"
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                     Library
                                                                                                                                                                                                        /clone_lib="LL19NC03 R chromosome 19-specific cosmid
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53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stilwagen, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arellano, A., Olsen, A.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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complement(54925611) complement(54925611) complement(54925611) conte-mps similarity to PID e255903 (277660) F38H4.7 [Caenorhabditis elegans]; (residues 209252); 72% [Caenorhabditis excellent, score: 95.000-DDS similarity frame: 2, quality: excellent, score: 95.000-DDS similarity to overlapping ESTs: [S5555492] T50998 yb71905.s1 Homo sapiens cDNA clone 76664 3' contains MER22 repetitive element; (344281); 92% identity-(56115492) W62177 md87d04.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 375367 5' similar to WP:T16H12.5 CE00510 KRUPPEL-LIKE ZINC FINGER PROTEIN; (35153); 84% identity-(55515492) T51086 yb71g05.r1 Homo sapiens cDNA clone 76664 5'; (160);100% identity.**		•	1862103		
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Xiang, M., Zhou, L., Macke, J.P., Eddy, R.L., Shows, T.B. and Nathans, J.
The Brn-3 family of POU-domain factors: Specific expression in subsets of retinal ganglion cells and somatosensory neurons unpublished
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                                                                                                                                                                                                                                                                                                                                  Submitted (25-MAY-1994) Mengqing Xiang, Dept. of Molecula
& Genetics, Johns Hopkins University School of Medicine,
Wolfe Street, Baltimore, MD 21205, USA
Location/Qualifiers
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USE OF NEURONAL APOPTOSIS INHIBITOR PROTEIN (NAIP)
Patent: WO 9726331-A 27 24-JUL-1997;
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/db_xref="taxon:32644"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding
/note="2 c 4 g 5 t
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligonucleotide"
2 c 4 g 7 t
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Sequence 52 1
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Sequence 16 from Patent W00100819
AX060375
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1 (bases 1 to 28)
Chauhan, S.
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                                                                                                                                       Patent: WO 0112833-A 52 22-FEB-2001;
E.I. DU PONT DE NEMOURS AND COMPANY (US) ; GENENCOR INTERNATIONAL,
                                                                                                                                                                                                                            synthetic construct
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1 (bases 1 to 28)
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                                                /organism="synthetic col/db_xref="taxon:32630"
/note="primer-primer"
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Sequence 112
AR210200
AR053365
Sequence 1 from patent US
AR053365
AR053365.1 GI:5978227
                                                                                                                                       10;
                                                                                                                                                                                                                                              Haugland, R. and Vesper, S.

Method of identifying and quantifying specific fungi
Patent: WO 0196612-A 112 20-DEC-2001;
PATES ENVIRONMENTAL PROTECTION AGENCY (US)
                                                                                                                                                                                                                                                                                                                      Paecilomyces variotii.
Paecilomyces variotii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae;
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Sequence 112 from Patent
AX402628
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Haugland,R. and Vesper,S.
Method of identifying and quantifying specific fungi and bacteria
Patent: US 6387652-A 112 14 MAY-2002;
Location/Qualifiers
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Similarity 76.9%;
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                                                                                                                                                                                          /organism="Paecilomyces variotii"
/db_xref="taxon:45996"
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Pred. No. 1.8e+05;
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l Similarity 76.9%;
l0; Conservative
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Lamb, C.J., Doerner, P. and Laible, G.
Purified palindromic element binding
Patent: US 6191258-A 1 20-FEB-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                     Unknown.
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Lamb,C.J., Doerner,P. and Laible,G.
AATT repeat transcription enhancer
Patent: US 5834236-A 1 10-NOV-1998;
Location/Qualifiers
1. 36
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AATT repeat transcription enhancer Patent: US 5834236-A I 10-NOV-1998; Incomparison of the control of the co
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Pred. No. 1.7e+05;
D; Mismatches 3;
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Pred. No. 1.7e+05;
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Sequence 1 :
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AR131089.1
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synthetic construct.
synthetic construct
artificial sequences
                                       A05096
Oligonucleotide L9 for salmon
A05096
A05096.1 GI:344983
                                                                                                                                                                                                                                                              synthetic construct.
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artificial sequences.
Location/Qualifiers
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Oligonucleotide U9 for
A04434
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Lamb,C.J., Doerner,P. and Laible,G.
Purified palindromic element binding
Patent: US 6191258-A 1 20-FEB-2001;
Location/Qualifiers
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/db_xref="taxon:32630"
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Sequence
AX204152
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 50)
Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorph.
methods of use thoreof
Patent: WO 0148245-A 259 05-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide
methods of use thereof
methods of use thereof
patent: WO 0148245-A. 258 05-JUL-2001;
                  Curagen
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Accession number cg43967861"
26
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/db_xref="taxon:9606".
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      Location/Qualifiers
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Search completed: December 26, 2002, 13:25:58 Job time : 2652 secs
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23 AATCAAACAATTA 35
                                                                                                                                                                                                                                   /note="single nucleotide polymorphism" 20 a 13 c 4 g 13 t
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
25. 26.
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43967861"
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RESULT 2 US-09-839-743-1

Sequence 1, Application US/09839743 Patent No. US20020146824A1

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; SEQ_ID NO 1
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; TYPE: DNA
; ORGANISM: Nicotiana tabacum
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Patent No. US20020146824A1
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PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/189,344
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/669,721
PRIOR FILING DATE: 1996-06-27
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/669,721
PRIOR FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 09/189,344
PRIOR FILING DATE: 1998-11-10
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CURRENT FILING DATE: 2001-04-19
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TITLE OF INVENTION: No. US20020146824Alel Transcription Enhancer Element and
TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof
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CURRENT APPLICATION NUMBER: US/09/839,743
CURRENT FILING DATE: 2001-04-19
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Best Local Similarity 76.9
Conservative
                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28

LENGTH: 44
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                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 28 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/839,743
CURRENT FILING DATE: 2001-04-19
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APPLICANT: Doerner, Peter
APPLICANT: Lable, Goetz
TITLE OF INVENTION: No. US20020146824A1e1
TITLE OF INVENTION: Transcription Factor
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 08/669,721 PRIOR FILING DATE: 1996-06-27
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                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/189,344 PRIOR FILING DATE: 1998-11-10
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                                 1 AATCAANNANTTA 13
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AATCAATTAATTA 17
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Laible, Goetz
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76.98;
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RESULT 6 US-09-777-564-743/c

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RESULT 8
US-09-969-373-1158/c
; Sequence 1158, Application US/09969373
; Patent No. US20020133852A1
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; LCCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or
US-09-783-590-1151
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1151
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APPLICANT: Haseltir
APPLICANT: Li, Haod
APPLICANT: Rosen, C
APPLICANT: Ruben, S
                                                                          GENERAL INFORMATION:
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SEQ ID NO 743
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Best Local :
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APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CHUDDENT AND THE TREE COLUMN AND THE TREE CHUDDENT AND THE TREE CHUDENT AND T
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493
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CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
APPLICANT: Effertz, Roger J. APPLICANT: Hauge, Brian M.
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Similarity 76.9%;
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Pred. No. 2.
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Pred. No. 2.1e+03;
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US-08-983-605-453/c
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SEQ ID NO 445
LENGTH: 78
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LENGTH: 99
SEQ ID NO 453
LENGTH: 20
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PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
                                                                                 CURRENT APPLICATION NUMBER: US/08/983,605A
CURRENT FILING DATE: 1998-05-01
EARLIER APPLICATION NUMBER: DE 195 25 284.5
EARLIER FILING DATE: 1995-06-28
                                                                                                                                                                    TITLE OF INVENTION: Microsatellite Markers for Plants of the Species TITLE OF INVENTION: Tailicum Aestivum and Tribe Triticase and the Use of TITLE OF INVENTION: Said Markers FILE REFERENCE: 2936.10400
                                         NUMBER OF SEQ ID NOS: 466
SOFTWARE: PatentIn Ver. 2.0
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Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
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76.9%;
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Pred. No. 2.1e+03;
0; Mismatches 3;
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Pred. No. 3.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 78;
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; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-452-599-39
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US-09-452-599-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-758-881-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us-09-758-881-20/c
                                                                                                                                                                                                                                         APPLICANT: Ouellette, Marc APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Specific TITLE OF INVENTION: Dathogen TITLE OF INVENTION: Specimen TITLE OF INVENTION: Specimen
                                                 SEQ ID NO 39
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09758881 Patent No. US20010029250A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/09452599 Patent No. US20020055101A1
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SEQ ID NO 20
LENGTH: 20
TYPE: DNA
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CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: PCT/US00/09054
PRIOR FILING DATE: 2000-04-06
                                                                                                               PRIOR FILLING FOR NUMBER: 08/3
PRIOR APPLICATION NUMBER: 08/3
PRIOR PRIOR DATE: 194-09-12
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/452,599
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 08/526,840
PRIOR FILING DATE: 1995-09-11
                                                                                      SOFTWARE:
                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/288,461 PRIOR FILING DATE: 1999-04-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Antisense (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Karras,
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                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Local Similarity 75.0%;
les 9; Conserva+:--
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9; Conserv
                                                                                      PatentIn Ver.
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                                                                                                                                                                                                                              ON: Specimens for Routine Diagnosis in Micro 12287.31
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                                                                                                                                                                                                                                                               Specific and Universal Probes and Amplification Primers to Rapidly Detect and Identify Common Bacterial Pathogens and Antibiotic Resistance Genes from Clinical
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2001-01-11
PCT/US00/09054
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75.0%;
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Pred. No. 7.5e
0; Mismatches
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Pred. No.
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. 7.5e+03;
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; OTHER INFORMATION:
US-09-835-371-46
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Best Local Similarity
"~+~hes 9; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/09860784 Patent No. US20020151512A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BREIPOHL, Gerhard
APPLICANT: WILL, David W
TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
FILE REFERENCE: 02481.1743 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/09/835,371
CURRENT FILING DAVE: .2001-04-17
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: UHLMANN, Eugen
APPLICANT: BREIPOHL, Ger
APPLICANT: WILL, David W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/09/860,784
FILING DATE: 21-May-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
OLASSIFICATION SATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AATCAATGACTT 13
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                               APPLICATION NUMBER: 08/594,452 FILING DATE: 04-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: G CAP-STABILIZED OLIGONUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PEYMAN, Anuschirwan
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9; Conserv
                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                  20007-5109
                  SANDERCOCK,
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75.0%;
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75.0%;
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Colin G.
3ER: 31,298
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Pred. No. 7.5e
0; Mismatches
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Pred. No.
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7.5e+03;
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APPLICANN: KAWAI, Shiji
APPLICANT: KAWAI, Shiji
APPLICANT: TO, Susumu
FITLE OF INVENTION: Gene for Enzyme Having Both Alkaline Pullulanase and Alkaline Alg
TITLE OF INVENTION: Amylase Activites
FILE REFERENCE: 2173-0122P
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US/10/014,436
CURRENT FILING DATE: 2002-05-10
PRIOR FILING DATE: 1995-05-10
PRIOR FILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR FILING DATE: 1996-05-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR FILING DATE: 1996-01-10
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR FILING DATE: 1996-01-10
PRIOR SEQ ID NO-02-28
NUMBER OF SEQ ID NO-92-28
NUMBER OF SEQ ID NO-514
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
ILENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
FEATURE:
OTHER INFORMATION: Primer 4. Directed to Bacillius sp. used between XbaI to 1.2 kb u
OTHER INFORMATION: pstream.
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INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-860-784-25
                                                                                                                            QΥ
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Search completed: December 26, 2002, 14:04:00 Job time: 57 secs
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US-10-014-436-10
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                                                                                                                                                                            Matches
                                                                                                                                                                                                 Query Match
Best Local :
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                                                                                     1 AATCAANNANTT 12
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12 AATCAAAGAATT 23
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Local Similarity 75.0%;
les 9; Conserva+:...
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TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGARASHI, Kazuaki
OZAKI, Katsuya
ARA, Katsutoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuji
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                                                                                                                                                                                               Score 9; DB 9; Length 24; Pred. No. 7.6e+03;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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      pathogen-specific promoter; infection; tissue-specific disease; clinherited disease; gene therapy; antimicrobial; multi-ribozyme; drug resistance; ARN promoter; ss.
                                                                                                                          AAZ58691 standard;
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Consider the particular targets delivery of ribozyme to the pathogen. Where compared cells and imposed containing (I) that include a pathogen. Where compared as antimicrobials, multi-ribozyme will not be affected by inherent compared to the custom delivery of ribozyme to the pathogen. Where compared as antimicrobials, multi-ribozyme will not be affected by inherent compared to the custom delivery of probably with a compared compared that several RNA targets (probably with a compared compared the compared to be selective for particular organisms; do not require a replicating delivery vehicle; are consisted in animal models. The present sequence represents a pseudomonas confirm invention of the invention.
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The invention relates to the discovery, identification and characterisation of toxic agents lethal to pathogen and methods for targeting such toxic agents to a pathogen or pathogen infected cells in order to treat and/or eradicate the infection. In particular the invention relates to at least one nucleic acid molecule, which separated with the transformation or plasmid copy number control, which associated with the transformation or plasmid copy number control, which hybridises to a viral polyadenylation signal or a core, pre core or hybridises to a viral polyadenylation signal or a core, pre core or copy polymerase encoding sequence. Specifically, the invention relates to the delivery of one or more toxic gene products, antisense RNAs, ribozymes, DARzymes or a combination thereof. The nucleic acids have antiviral activity and can be used in gene therapy. They are useful for the treatment of papilloma or hepatitis virus induced conditions and can produce a cytotoxic or cytostatic effect in papillomavirus or hepatitis B
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Parkinson's disease; Alzheiner's disease;
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                                                                 cation/Qualifiers
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                      Brn_3a_polypeptide
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                     cells; apoptosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCGCCTGCTCGGCGGTGCCGGTCCGTG
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                                                                                                                                                                                                                                                                                                       cell death;
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                                                                                                                                                                                                                                                                                                       CNS;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                      neuron specific manner and consequent protection of neuronal cells from apoptosis suggests that Brn-3a may co-ordinate some aspects of neuronal reorganisation during development or following injury. The elevation of Brn-3a expression by either pharmacological means (compositions comprising one other therapeutic polypeptide e.g. neurotrophic factors, nerve growth factor (NGF), cillary neurotrophic factor (CNTF), brain-derived neurotrophic factor (BNTF), and neurotrophins NT-3 and NT-4/5) or gene therapy may represent a method for treating human diseases associated with excessive neuronal cell death and/or lokk of herve regeneration, especially neurodegenerative diseases such as familial dysautonomia and infantile muscular dystrophy, and Parkinson's and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Over expression of transcription factor Brn-3a can protect neuronal cells from apoptosis. Brn-3a also specifically activates expression of the BCl-2 gene in neuronal cells and this activation is mediated via a Brn-3a response element in the 5' regulatory region of the Bcl-2 gene. Both the anti-apoptopic effect of Brn-3a and its ability to activate expression of Bcl-2 are mediated by the N-terminal domain of Brn-3a. Members of the Bcl-2 family perform critical roles in the regulation of selective apoptosis during development of the nervous system. The stimulation of Bcl-2 expression by Brn-3a in a
             AAA29006
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1272
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25-JUL-1997;
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nes 118; Conser
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               standard;
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               cDNA; 1272
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Best Local :
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                                                                                                                                                                                                                                              Sequence 1272 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Product for treating, preventing and diagnosing cervical ca
comprises a nucleotide sequence or molecule which binds to
decreases its intracellular levels or inhibits its activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Latchman DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-1998;
31-MAR-1999;
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            GGCCTTGGCGTCCGCGGCGCGCGCGTGATGAGGGCGGCACCTGGGTGATCCAG
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DB; AAY96404.
antisense;
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99US-0282210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product= Brn-3a_transcription_factor
                                                                                                                                                                                                                                             202 A; 468-C; 452 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitor; cervical cancer; human
                                                                                                                                                                                                          9.7%;
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Pred. No. 0.
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14-APR-2000;
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                                                                                                                                                                                                                                                                  (SINV-)
                                                                                                                                                                                                                                                                                                        (SNTF )
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AAD17186 standard; DNA; 125401 BP.
New nystatin polyketide synthase
                                     AAE10149,
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                                                                                                                                                                 ) ZOTCHEV S B.
) SEKUROVA O N.
) FJAERVIK E.
) BRAUTASET T.
) STROM A R.
                                       AAE10143, 1
9, AAE10150.
                                                                                                           SB, Sekurova
, Ellingsen TF
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                                                                                                                                                                                                                                                                                        SINVENT AS.
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51155..57355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product "NysL protein" complement (58786..58980)
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/product= "NysK
57503..58687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /"Lag" g
/product= "NysD2 complete protein"
120628..121308
/*+>~ '
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/product= "NysI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "NysN protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product= "NysR4 (long) protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product= "Nysm protein"
                                                       AAE10144, AAE10145,
                                                                                                               TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nystatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKS; macrolide; nystatin;
                                                                                                                               Š,
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                                                                                                               Sletta
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                                                                                                           Fjaervik E, Brautaset
letta H, Gulliksen O;
                                                                                                                                                                                                                                                                                                                              TEK FORSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKS gene cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete protein"
polynucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      include
                                                       AAE10146, AAE10147, AAE10148
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polypeptides
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AAH41550/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44196 CGGTACCGCGTCGTCGCCGCTCGTCTCGTCGAGCGCGAGCAGGGAGACCACGGCGGTCGG 44137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44136
                                                                                                                                                                                                                                                                                       Mouse; human;
2-3 type zinc
gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (FKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present
                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                  Human Rit1 gamma nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful as antibiotics and antifungals
         therapy
           New zinc finger protein and gene encoding it for detecting diagnosing cancer, estimating the risk of carcinogenesis, atherapy
                                                 WPI; 2001-316438/33.
P-PSDB; AAB99341.
                                                                                  Kominami
                                                                                                                          29-OCT-1999;
                                                                                                                                                14-JUL-2000;
                                                                                                                                                                      10-MAY-2001.
                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                          WO200132859-A1
                                                                                                     (MOCH ) MOCHIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is a Streptomyces noursei nystatin PKS gene cluster DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 188-254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                2000WO-JP04765
                                                                                                                                                                                                                                                                                           зb
                                                                                                                                                                                                                                                                                                  combined DNA/RNA molecule;
finger structure; cancer; c
                                                                                                                           99JP-0310420
                                                                                                     PHARM CO LTD
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                               /product= "Rit1 gamma"
                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                       44003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.5%;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                   diagnosis;
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. 26;
                                                                                                                                                                                                                                                                                                             Rit1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                             tumour suppressor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 125401;
                                                                                                                                                                                                                                                                                                   carcinogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
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                for gene
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Claim

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Page

81-84; 119pp; Japanese.

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 112
diagnosing therapy -
                                                           WPI;
         New zinc finger protein and gene encoding it for detecting diagnosing cancer, estimating the risk of carcinogenesis, \boldsymbol{\epsilon}
                                                                                                                                                                                                                                                                                                                                                                                                                               AAH41549 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a combined DNA/RNA molecule designated Rit1, which has a 2-3 type zinc finger structure and tumour suppressor activity. Rit1 has cytostatic activity and can be used in gene therapy. Genomic or cDNA encoding Rit1 can be used in the detection and diagnosis of cancer, and the estimation of the risk of carcinogenesis. Rit1 and its partial peptides are also used to detect and diagnose cancer, and estimate the risk of carcinogenesis. The present sequence encodes
                                              P-PSDB;
                                                                                   Kominami
                                                                                                                                                                               10-MAY-2001.
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                                                        (MOCH )
                                                                                                                                29-OCT-1999;
                                                                                                                                                      14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                   Mouse; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            892
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                                                                                                                                                                                                                                                                                                                       type zinc
                                                           2001-316438/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy;
                                                                                                                                                                                                                                                                                                                                                        Ritl beta nucleotide sequence
                                                AAB99340.
                                                                                                        MOCHIDA
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                                                                                                                                                                                                                                                                                                             ds.
                                                                                                                                                                                                                                                                                                                     combined DNA/RNA molecule; Ritl; tumour suppressor;
finger structure; cancer; diagnosis; carcinogenesis;
                                                                                                                                99JP-0310420
                                                                                                                                                                                                                         Location/Qualifiers
11..2482
/*tag= a
/product= "Rit1 beta"
                                                                                                        PHARM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531 A; 925 C; 863 G;
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%;
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                                                                                                                                                                                                                           "Ritl beta"
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Pred. No. 0.24;
0; Mismatches
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           gene
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RESULT 9
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Matches
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                                                                                                                                                                                                                                   Key
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                               P-PSDB;
                                                                                                                                                                                     WO200132859-A1.
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       Human Ritl alpha' nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its partial peptides are also used to detect and diagnose cancer, estimate the risk of carcinogenesis. The present sequence encodes
                                                                    Kominami R;
                                                                                                                 29-OCT-1999;
                                                                                                                                      14-JUL-2000; 2000WO-JP04765
                                                                                                                                                              10-MAY-2001.
                                                                                                                                                                                                                                                                                                  2-3 type zinc
                                                                                                                                                                                                                                                                                                                 Mouse; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-316438/33
                                                                                                                                                                                                                                                                                       therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCGGCACCTGGGTGGTGATCCAGCCACTGAGGGTCAACAT 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCAGTAGCAGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCGGCTCGTG 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGGCCGGCCAGCGAGCCGGCCTTGTGCATGTGCGTCTTCAT 1217
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                                AAB99339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                   combined DNA/RNA molecule; Ritl; tumour suppressor; finger structure; cancer; diagnosis; carcinogenesis
                                                                                                                                                                                                                                                                                          ds
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                             3332
                                                                                                                                                                                                         "Ritl alpha'"
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Pred. No. 0.24
0; Mismatches
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                                                                                                                                                                                                                                                                                                     carcinogenesis;
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diagnosing cancer,

New zinc finger protein and gene encoding diagnosing cancer, estimating the risk of

it for detecting carcinogenesis,

for

gene

for detecting

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ARESULT 10
AAH4155/c
ID AAH415
XX
AC AAH415
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                                              P-PSDB;
                                                                                                                                                                                                                                                   14-JUL-2000;
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2-3 type zinc
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le therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1471
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                                               Uniform amplification of heterogeneous mixture of nucleic acid templates of varying G+C content, comprises amplifying the reamixture in the presence of betaine and dimethyl sulphoxide -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211
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RESULT 12
AAV33912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     octamer binding protein OCT-T1. It was used as a test sequence in an CC assay to demonstrate the method of the invention, which involves a novel CC way of amplifying GC rich nucleic acids. In addition to the normal CC mixture a zwitterion and a compound which disrupts base pairing are added CC to the PCR reaction. The zwitterion is preferably betaine (trimethyl CC glyche), D-carnitine, dimethyl glycine or monomethyl glycine, and the CC base pair disruption compound may be DMSO, formamide, sodium perchlorate CC or glyoxyl, among others. This method is useful as it allows the uniform CC and more efficient amplification of nucleic acids composed of GC rich CC regions. This is useful in DNA library construction, as the 5' end of CC genes are often GC rich, and in the diagnosis of diseases where GC rich CC muscular atrophy, myotonic dystrophy, Huntington's disease and XX spinocerebellar ataxia type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local
                                                                                                                                                                                                                                                                                                      Nucleotide sequence of the SIAX DP2-64 (Oct-T1) gene
WPI; 1999-009425/01
                        Boon-Falleur T,
                                                                          25-APR-1997;
                                                                                                   22-APR-1998;
                                                                                                                            05-NOV-1998
                                                                                                                                                     WO9849299-AJ
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                        SIAX
                                                                                                                                                                                                                                                                 Tumour rejection antigen precursor; TRAP; TRH; leukaemia; lymphoma; cancer; HLA; human lymphocyte antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                12-FEB-1999
                                                                                                                                                                                                                                                                                                                                                         AAV33912;
                                                                                                                                                                                                                                                                                                                                                                                  AAV33912 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 530 BP; 61 A; 215 C; 203 G; 51 T; 0 other;
                                                 (LUDW-) LUDWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 TCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCCATGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGCGCGATGAGGGCGCCACCTGGGTGG
                                                                                                                                                                                                                                                     DP2-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGCCGGGCGGCGGCTCCTGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGCCAGCTCGCGCCTGCCTGGGAAAGCTGTACATGCTG-ATCGGCGGCGTCGGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                     Oct-T1; ss.
                                                                                                                                                                                                                                                                                                                                (first
                                                 INST CANCER RES
                                                                          97US-0845998
                                                                                                   98WO-US07784.
                                                                                                                                                                                       Location/Qualifiers
174..1436
                        Coulie
                                                                                                                                                                                                                                                                                                                                                                                  cDNA; 4524
                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.38;
                        'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                        Smet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
                        Lucas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Length 530;
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                        Van Baren
                                                                                                                                                                                                                                                                             screening;
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AAQ83793/c
ID AAQ837
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 113;
           Denoya
                                                                                    30-MAY-1994;
                                                                                                            09-FEB-1995.
                                                                                                                                                                                                         Streptomyces avermitilis.
                                                                                                                                                                                                                                   nematocide;
                                                                                                                                                                                                                                              Branched-chain alpha-keto-acid-dehydrogenase; BCKDH; bkd gene; avermectin; antibiotic; acaricide; anthelmintic; insecticide;
                                                                                                                                                                                                                                                                                  S. avermitilis
                                                                                                                                                                                                                                                                                                          05-SEP-1995
                                                                                                                                                                                                                                                                                                                                                          AAQ83793 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the nucleotide sequence of the SIAX DP2-64 (Oct-T1) gene. The protein is a tumour rejection antigen precursor (TRAP). The specification describes the treatment of disorders which characterised by expression of a leukaemia-associated nucleic acid such as TRH. The products are used for in vivo or in vitro screening for leukaemia, lymphoma or other cancers by usual hybridisation/amplification or immunoassay methods. TRAPs, when processed to antigens or complexed with HIA (human lymphocyte antigen) molecules, or nucleic acid encoding them, are useful in vaccines for received.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW68541
                                   (PFIZ ) PFIZER
                                                            30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Pages 63-67; 88pp; English.
                                                                                                                                   WO9504150-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4524 BP; 1177 A; 1090 C; 1180 G; 1077 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New diagnosis of leukaemia - by detecting genes for tumour antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating
                                                                                                                                                                                                                                                                                                                                                                                                                       703
                                                                                                                                                                                                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 TCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCCATGGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      GCGGCCCGGGCGGCGGCTCCTGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGCGCGATGAGGGCGCCACCTGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCCAGCTCGCGCCCTGGCAAAGCTGTACATGCTG-ATCGGCGGCGTCGGTGCCG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursors or corresponding proteins
                                                                                                                                                                                                                                  pesticide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                        (first entry)
                                                            9308-0100518
                                                                                    94WO-IB00127
                                                                                                                                                                                                                                                                                 BCKDH E1-alpha subunit.
                                                                                                                                                                       Location/Qualifiers
1..1146
                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                           cDNA; 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45.6; DB Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4524;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     702
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  RESULT 14
AAQ83797/c
ID AAQ83797 standard; cDNA; 2728
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    were obtained. A genomic sequence including the E1-alpha, E1-b and E2 (partial) bkd ORFs was also isolated (AAQ83797). Manipu of bkd genes allows the enhanced production of natural or novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel branched chain alpha-keto-acid-dehydrogenase (BCKDH) genes (bkd) from Streptomyces avermitilis were cloned using PCR and homology probing. DNAs encoding the BCKDH El-alpha, El-beta, an N-terminal and internal portions of the E2 subunit (AAQ83793-96)
                    CDS
                                                                     CDS
                                                                                                                       CDS
                                                                                                                                          RBS
                                                                                                                                                                                                     Branched-chain alpha-keto-acid-dehydrogenase; BCKDH; bkd gene avermectin; antibiotic; acaricide; anthelmintic; insecticide;
                                        RBS
                                                                                        RBS
                                                                                                                                                                         Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 42; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to improve prodn. novel avermectin cpds
                                                                                                                                                                                            nematocide;
                                                                                                                                                                                                                                                        05-SEP-1995
                                                                                                                                                                                                                                                                            AAQ83797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1146 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces branched-chain alpha-keto-acid dehydrogenase DNA used to improve prodn. of natural avermectin cpds and to produce
                                                                                                                                                                                                                                                                                                                                                   622
                                                                                                                                                                                                                                                                                                                                                                                         682
                                                                                                                                                                                                                                                                                                                                                                                                                                 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
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                                                                                                                                                                                                                                    avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995-082233/11.
DB; AAR69623.
                                                                                                                                                                                                                                                                                                                                                                      TCCAG 236
                                                                                                                                                                                                                                                                                                                                                                                        CGGCCTTGTGGGCCAGCGACGGGGGGGGCGGCGGTCTGCTTGGCGAGCGGGACGGAGATGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                          CGGTCCGTGCGGCCTTGGCGTCCGCGGGGGCGCGCGCATGAGGGCGCGCACCTGGGTGA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
97; Conserv
                                                                                                                                                                                           pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                         avermitilis
                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                  bkd gene region
                                                                                                                    /*tag= a
403..1548
        /*tag= e
2626..2728
/*tag= f
                                      /*tag= d
/product= E
2610..2615
                                                                                       /product= F
1607..1614
                                                                                                                                           390..395
/product=
                                                                    .622..2626
                                                                              /*tag=
                                                                                                            /*tag= b
                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 A; 465 C;
                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.0%;
52.4%;
E2
                                                 E1-beta
                                                                                                  E1-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44.2; DB Pred. No. 0.55;
N-terminal
                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 G; 126 T; 0 other;
                                                 subunit
                                                                                                   subunit
sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cpds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E1-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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                                                                                                                                                                                                                                                                                                                                                                                        623
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RESULT 15
ABV23346
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bkd) from Streptomyces avermitilis were cloned using PCR and homology probing. DNAs encoding the BCKDH E1-alpha, E1-beta, an N-terminal and internal portions of the E2 subunit (AAQ83793-96) were obtained. A genomic sequence including the E1-alpha, E1-be and E2 (partial) bkd ORFs was also isolated (AAQ83797). Manipul of bkd genes allows the enhanced production of natural or novel
                                                                                                                                                                                                                            1024
                                                                                                                                                                                                                                                                    1084
                                                                                                                                                                                                                                                                                                               1144
                                                                                                                                                                                                                                                                                                                                                         1204
                                                                    Human; prostate pharmacogenomic
                                                                                                                                                ABV23346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces branched-chain alpha-keto-acid dehydrogenase DNA -used to improve prodn. of natural avermectin cpds and to produce
                                                                                                     Human prostate expression marker cDNA 23337
                                                                                                                            16-SEP-2002
                                                                                                                                                                     ABV23346
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel avermectin cpds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR69623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-082233/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denoya CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9504150-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PFIZ )
                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                                                               232
                                                                                                                                                                                                                                                                                                                                                                           CCTCGTGCACGGCCGCCGCGTCGTTGCCGTCGACCAGGCGGCCCGGCATCCCGTAGCCGA
                                                                                                                                                                                                                                                                                                                         GTACATGCTGATCGGCGGCGTCGGTCGCCGGCCGGCCCTGCCTCGCCTGCCTCGCCTGC 171
                                                                                                                                                                                                                           AGCCG
                                                                                                                                                                                                                                                TCCAG
                                                                                                                                                                                                                                                                   CGGCCTTGTGGGCCAGCGACGGGGCGGCGGCGCTCTGCTTGGCGAGCGGGACGGAGATGGCGA 1025
                                                                                                                                                                                                                                                                                         CGGTCCGTGCGGCCTTGGCGTCCGCGCGCGCGCGCATGAGGGCCGCCACCTGGGTGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         branched-chain alpha-keto-acid-dehydrogenase (BCKDH) genes
                                                                                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFIZER
                                                                                                                                                                     standard; cDNA; 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                            2728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 44-45; 65pp;
                                                                                                                                                                                                                           1020
                                                                                                                                                                                                                                               236
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0100518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94WO-IB00127.
                                                                    cancer; cytostatic; carcinogen;
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR69624;
                                                                                                                                                                                                                                                                                                                                                                                                                                           388 A; 1005 C;
                                                                                                                                                                                                                                                                                                                                                                                                            9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                Score 44.2; D
Pred. No. 0.62
0; Mismatches
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                                                                                 pharmacodyanamic marker;
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WO200160860-A2 Homo sapiens

20-FEB-2001;

2001WO-US05171.

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Best Local Similarity
Matches 118; Conserv
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                  1328
                                                                                                                                   1268
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1388 BP; 205 A; 445 C; 377 G; 338 T; 23 other;
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                 GGCGTCGGTGCCGGCCGGGTCTTCCGCCTGCT-CGGCGGTGCCGGTCCGTGCGGCCT 186
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gb_htc: *
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AL053013 Drosophil
AL1.08460 Drosophil
BG487612 EM1_65_B1
BF266741 HV_CBa001
BE426427 WHE0335_H
AL547921 AL547921
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ALIGNMENTS

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AL053013
AL053013.1 GI:4934461
EXEMPOREDS
SOURCE
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilade;
Drosophila melanogaster
DOURNAL
Direct Submission
Direct Submission
Direct Submission
Determination of this BAC-end sequence was carried out as part of a melanogaster genome using these BACs. For further information
The BDGP is constructing a physical map of the Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Enancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial

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ACCESSION
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AL108460
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project grant. The DI and Genevieve Payan. pBeloBAC11.
                                 - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    fly), genomic AL108460
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                                                                                                                                                                                                                                 Direct Submission
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/db_xref="taxon:727"
/clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCTGTACATGCTGATCGGCGGCGTCGGTGCCGGGGGCCGGGTCTTCCGCCTGGTCTCGGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKSBTSBSSBSTSSSASBSSSSSSSSSSSTSTTBSTSBBBSTSSSSSGSSSSSBBSTBSBS 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSTSSGTTCGBCSSTGGCSCCCYCSCCCTCSTCGTSTCCSCSCSGTGSSBKCCYSTSSSA 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGATCCAGCCACTGAGGGTCAACATTCCAGTCACTCCGGGAAAAATGGAATTCTTCCA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTSKCSTBTSGSTBTSTBMSKBSSTSSTSBTSGSSBCGGSCGSTSGSSCSSBCGKSTSS 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
BG487612
BG487612.1
                                                                                                                                                                     Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                        High quality sequence
                                                                    Seq primer: PolyTMix
                                                                                                 Sequences have been below Phred quality
                                                                                                                                                                                                                            Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and An EST database from Sorghum: developing embryos Unpublished (2000)
                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                 sorghum.
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                              EST.
                                                                                                                                                                                                                                                                                                                                                                                                                   BG487612 553 bp mRNA linear EST 27-W
EM1_65_B11.g1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
                                                                                      is 20
                                                                                                                           Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                     clade; Panicoideae; Andropogoneae;
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706 583 0210
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Location/Qualifiers
1. .553
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/plasmid="pBeloBAC11"
/note="end : SP6"
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/db_xref="taxon:7227"
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17.2%;
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16. The
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hest quality
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REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCACGGGCTCGCCGTCGGACCTCGGCCCAGACGTGGGCGACGAGCTCGGCGCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCTTGGCGTCCGCGGCGCGCGCGATGAGGGCGCACCTGGGTGGTGATCCAGCCACT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGGTGACGTCGTTGAGGTCCGCGGGGGCGTCCCCCGCGGCGGCGGCGCCCACGGGCCACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147;
                                                                                                                                                                                                                                             Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla13) seedling leaf cDNA [library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF266741 523 bp mRNA linear EST HV_CEA0015024f Hordeum vulgare seedling green leaf EST HV_CEA0004 (Blumeria challenged) Hordeum vulgare cDNA cHV_CEA0015024f, mRNA sequence.
                                                                                                                                  Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                              Clemson University Genomics
                                                                                                                                                                                                   Contact: Wing RA
                                                                                                                                                                                                                           On Nov 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF266741.2 GI:13262953
                                            Total hq bases - 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare.
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                                                                                                                                                                                                                                                                                                                                                                                                       Triticeae; Hordeum. (bases 1 to 523)
  primer: AATTAACCCTCACTAAAGGG
                                                                 864 656 7288
864 656 4293
1: rwing@clemson.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Torgan: Embryos germinated for 24 hr; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: ECORI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."

179 c 218 g 74 t
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/db_xref="taxon:4558"
/clone_lib="Embryo 1 (EM1)"
                                                                                                                                                                                                                        2000 this sequence version replaced gi:11197736
sequence
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Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                           291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
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                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CGCGGATCATCTTCACCATCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCCA 63
                                                                                                                                                                                                                                                                                                                                       CCTTGGCGTCCGCGGGGCGCGCGTGATGAGGGCGGCACCTGGGTGGTGATC
                                                                                                                                                                                                                                                                                                                                                                                         NTACTCCATCGCCTCGGAATTCGTGGTCACGGCCACGACGGTGCCGAGGTTCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGCTCCGGCTTGGCCGCCGCCGACCGCCGACACGGCCTATCCGCCTCCTACGACCCGCG
                                                                                              BE426427
610 bp mRNA linear EST 24-JUL-WHE0335_H02_P03ZS Wheat unstressed seedling shoot cDNA library Triticum aestivum cDNA clone WHE0335_H02_P03, mRNA sequence.
BE426427
Triticum aestivum
                                                                          BE426427.1
                             bread wheat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (C.I. 16155 (Mal3) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate A27 (AvrMla13) of Blumeria graminis f. sp. hordel, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence above. For more details on library preparation and seminence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)* 156 c 210 g 67 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence analysis see
http://www.genome.clemson.edu/projects/barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this clone see http://www.genome.clemson.edu/orders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
/cultivar="CI16155 (Mla13)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="seedling green leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Hordeum vulgare seedling
library HVcDNA0004 (Blumeria challeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4513"
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                                                                             GI:9424270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%;
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Pred. No. 0.
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challenged)"
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Viridiplantae;

Streptophyta; Embryophyta; Tracheophyta;

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RESULT 6
AL547921/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                           92
                                                                                                                                                                                                                                                                                                                                                                                                         32 CTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCCATGGTAGCGGCCAGCTC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                     AGACGAAAGCGAAAGAGGAACGAAGCCGCAGA 331
                                                                                                                                                                                                                                       TTCCGCCTGCTCGGCGGTGCCGGTCCGTGCGGCGCGTTGGCGTCCGCGCGCGCGCGCGCGATGA 211
                                                                                                                                                                                                                                                                                                      GGCATCTGCCTCCGCCTGCGTCATGCTCGCCGTCGATCCCGTCGGCGGCGTCGGCGGCGGA
                                                                                                                                                                                                                                                                                                                            prime, mRNA
AL547921
AL547921.1
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsda,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

The structure and function of the expressed portion of the wheat
                                                             AL547921 LTI_NFL006_PL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
, germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Shoots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
                                                 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other authors)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Wheat unstressed seedling shoot cDNA library"
/tissue_type="Etiolated shoot"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Five day old seedling"
/lab_host="E. coli SOLR"
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Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 610;
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)1033YH07 3
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Best Local
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                                                                               AUTHORS
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GSGGSSSSSTSCSTSGTCKCKKCCKKKCGSCGGGSKCGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGSSCTYGSCSTYCTCCSKSCSSTTCTCCSCBSCTSSTTTCKSTGSYCTCCCCYCSSCKS 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCGGATCATCTTCACCATCGGCCGCAACTCCTGCGGGGATATCCTCGTCCTCCTCCA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGGGTGTGGGCKGGSSSSKCGSSSKTSCKCKKSSGSSSSKSKSKSSKKSCKSSCSS
                                                                                                                                              Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
Spermatophyta; Magnollophyta; Sorghum.
              An EST database from Sorghum: pathogen-induced Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                            PI1_69_E06.b1_A002 Pathogen mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li,W
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                                                                                                                Cordonnier-Pratt, M. - M., Gingle, A.,
                                                                                                                                                                                                                                                              sorghum
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                                                                                                                                           (bases 1 to 332)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pcW/SPORT 6; Site_1: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcW/SPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://fulllength.invitrogen.com"
170 c 238 g 23 t 15
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 0.
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Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 66;
                                                                                                             Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGGCGCCGGCCATGCCGGCCCGGCACGACGAAGTCGAACTGCTGGCCGGCGGCGGCGAC 205
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                                                                                                                                                                                                                                                                                                                                                                                                  BF485240

BF485240

WHE1790_All_B22ZS Wheat pre-anthesis spike cDNA library Triticum cDNA clone WHE1790_All_B22, mRNA sequence.
Anderson, O.D., Ch., P.S., Hsia, C.C.,
                                                                                                           Spermatophyta; Magnoliophyta;
; Triticeae; Triticum.
                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                  Triticum aestivum
                                                                                                                                                                                                                                                                                                                                 BF485240.1 GI:11568541
                                                                                                                                                                                                                                                                                                                                                                            BF485240
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYA-No.
                                                                                                                                                                                                                                                                bread wheat.
                                                                        (bases 1 to 190)
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two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
cultivar) were infected with pathogen (isolate FRW42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptiblity
to anthraconose disease. The library was made from poly-A
num in the closer of the second of the content of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Pathogen induced_1 (PII)"
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1. .332
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107 c
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51.9%;
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Building, Rm. 2502, Athens, GA 30602-7271, USA
                                  Chao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or all ESTs are expected to derive from the host no effort was made to eliminate ESTs deriving from
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Pred. No. 0.59;
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Y., Lazo,G.R.,
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Close,T.J., F
R., Miller,R.,
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                                  Fenton, R.D.,
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BG356596
BG356596.1
EST.
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
And Bunchanan Street, Albany, CA 94710, USA
Plant Sciences Building,
Tel: 706 542 1860
Fax: 706 583 0210
                                   Laboratory for Genomics and Bioinformatics The University of Georgia, Department of P. Plant Sciences Building, Rm. 2502, Athens,
                                                                                                            An EST database from Sorghum: Unpublished (2000)
                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                      Reid
                                                                                                                                                                                                                                                Sorghum bicolor
                                                                                                                                                                                                                                                                    sorghum.
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Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                          Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 5105595818
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id,S.P., Cordonnier-Pratt,M.-M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     greenhouse. Whole spike with awns trimmed, white, greenhouse and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and poly(A) RNA were prepared.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: XhoI; Plants were grown in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preparations and DNA sequencing were performed Anderson lab (all other authors)."
67 c 70 g 27 t
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Location/Qualifiers
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/tissue_type="Spike before anthesis"
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                                   Department of Plant Biology m. 2502, Athens, GA 30602-7271, USA
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                                                                                                                                            unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
Tel: 706 542 1860
Fax: 706 583 0210
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Sequences have been trimmed
below Phred quality 16. The
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                                                                               Sequences have been trimmed below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 529)
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                                          Seq primer: T7
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Sorghum bicolor
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quality sequence start: quality sequence stop:
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                                                                                                                         mmpratt@uga.edu
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/note="Organ: Embryos germinated for 24 hr; Vector:
Site_1: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
121 c 146 g 63 t
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/db_xref="taxon:4558"
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Pred. No. 0
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                                                                           to exclude PolyA, vector and regions threshold for highest quality sequence
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JOURNAL
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Best Local Similarity
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                                                                                                                                                                                                                                                   Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AW747229
AW747229.1 GI:7660967
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                                                                                                                                          is 20.
Seq primer: T7
                                                                                                                                                                       Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                        Tel: 706 542 1860 Fax: 706 583 0210
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 536)
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/Clone_lib="Water-stressed 1 (WS1)"
/note="Organ: M1x of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
a 140 c 177 g 116 t
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants
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/db_xref="taxon:4558"
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threshold for high
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RESULT 12
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                   High quality sequence
                                                                                                                                                                                                                                                                                                       Email: mmpratt@uga.edu
Sequences have been tr
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Similarity 51.9%;
07; Conservative
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_52_A04.g1_A002 Water-stressed 1 (WS1) Sorghum bicolor
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a 144 c 178 g 117 t
                ß
        /clone_lib="Water_stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
153 c 207 g 114 t 1 others
                                                                                                                                 /organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                   ocation/Qualifiers
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107; Conserv
                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW678141
AW678141.1
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                                                                                                                                                                                                                                               High quality sequence
                                                                                                                                                                                                                                                                                                                       Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                    Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clade; Panicoideae; Andropogoneae;
1 (bases 1 to 617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                Similarity
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   Conservative
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                                                                  /Clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
/mater was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
a 162 c 215 g 123 t
                                                                                                                                                                         organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                        ave been trimmed quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:7551863
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Water-stressed 1
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               Score 47.6;
Pred. No. 0
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617
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threshold for high
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1 (WS1) Sorghum bicolor
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30602-7271,
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                                                                                                                                        Local Similarity
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                                                                              CGCGGATCATCTTCACCATCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCA 63
GCGTGCCGATACCCACGCCGCGGGGC 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:Chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                         end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AG162326 803 bp DNA linear GSS 09 Pan troglodytes DNA, clone: RP43-028L15.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                             Sequencing: TJ
LIBRARY
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                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                             Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
                                                                                                                                                                                                         56
                                                                                                                                                                                              /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
/clone_13 c 456 g 15 t 33 others
                                                                                                                                                                                                                                                 /clone="RP43-028L15.TJ"
/sex="male"
                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  . 803
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Pred. No. 1;
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                         CCAGTCAC 262
                                                                                                       AGCAGCCCGTGCCACTCCGTGACGACGACGGTGACGGTGAGCTCGCCGTCCGCGGCC
                                                                                                                                                          ATGGTGGCGAGGCGAACGCGGCCGCCGCCGGCGGCAGCGCGGCGCACACCCGGCGAGGCC 369
GCGACCAC
                                                    GCGAGGAGGCGGCACGCGGCCAGCATCGGGTTGATGTGGCCGGGCCCGGGTACGGCACC
                                                                            GCGGCGCGCGCGATGAGGGCGCACCTGGGTGGTGATCCAGCCACTGAGGGTCAACATT 254
                                                                                                                                 GTGCCGGCCGGCTCTTCCGCCTGCTCGGCGGTGCCGGTCCGTGCGGCCTTGGCGTCC 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rdean@clemson.edu
Seq primer: T3 primer (AATTAACCCTCACTAAAGGG)
High quality sequence stop: 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson Universiy, Clemson,
Tel: 864 656 5737
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rauyaree,P., Choi,W., Fang,E., Blackmon,B.
Genes expressed during early stages of rice
blast fungus Magnaporthe grisea
Mol. Plant Pathol. 2 (6), 347-354 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW155496 697 bp mRNA linear EST 03 mgie0026009f Rice blast infection stage cDNA library Oryza sativa/Pyricularia oryzae mixed EST library cDNA clone mgi
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Oryza sativa/Pyricularia oryzae mixed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; mixed
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                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: LOTELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
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ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
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ATTORNEY/AGENT INFORMATION:
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LOCATION:
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54.38;
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                                                                                                                           Score 45.6; DB 2; Pred. No. 0.072;
                                                                                                                Mismatches
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US-09-206-537-7
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4524 base pairs
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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82 CGGCCAGCTCGCGCCCTGCCTGGGAAAGCTGTACATGCTG-ATCGGCGGCGTCGGTGCCG 140
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02210
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                                                                                                                                 Score 45.6; DB Pred. No. 0.072; 0; Mismatches
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                                                                                                                             Query Match 9.3%;
Best Local Similarity 54.3%;
Matches 113; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                     22 TCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCCATGGTAG 81
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                          CGGCCAGCTCGCGCCCTGCCTGGGAAAGCTGTACATGCTG-ATCGGCGGCGTCGGTGCCG 140
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TD NO: 7:
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Lucas, Sophie
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                                                                                                                             Score 45.6; DB 4;
Pred. No. 0.072;
0; Mismatches 94;
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US-08-482-385A-1/c
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SHEYKA,, ROBERT F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                       Local
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AGCCG
                          TCCAG 236
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97; Conserv
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235 EAST 42ND STREET, 20TH FLOOR
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GENES ENCODING BRACHED CHAIN ALPHA
KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES
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Pred. No. 0.13;
0; Mismatches 88.
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US-08-482-385A-5/c ; Sequence 5, Application US/08482385A

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                                                                                                                                                               GENERAL INFORMATION:
                                                  APPLICANT: Leopardi, Rosario APPLICANT: Roizman, Bernard TITLE OF INVENTION: HERPES SIM TITLE OF INVENTION: INHIBITOR (NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-573-1939
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: SHEYKA, ROBERT F.
REGISTRATION NUMBER: 31,304
REFERENCE/DOCKET NUMBER: PC83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212.573-1189
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APPLICANT: DENOYA, CLAU
TITLE OF INVENTION: GENE
TITLE OF INVENTION: KETC
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 GTACATGCTGATCCGGCGCGCGTCCGGCCGGCGCGGGTCTTCCGCCTGGCCGGTGC 171
                                                                                                                                                                                                                                                                                                                              232 TCCAG 236
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ZIP: 10017-5755
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CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/482,385A FILING DATE: 07-JUN-1995
                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 9.0%;
Local Similarity 52.4%;
Les 97; Conservative
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                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                   CGGTCCGTGCGGCCTTGGCGTCCGCGGCGGCGCGATGAGGGCGGCACCTGGGTGGTGA 231
SEE: Arnold, Wh
: P.O. Box 4433
Houston
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                                                                                      Bernard
HERPES SIMPLEX VIRUS ICP4 AS
INHIBITOR OF APOPTOSIS
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Best Local S
Matches 107
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REFERENCE/DOCKET NUMBER: ARCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                 SOFTWARE:
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                  Query Match
 Matches 107;
                     Best Local Similarity
                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 08/690,473
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/259,821A CURRENT FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                   APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS
                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                           LENGTH: 4257
TYPE: DNA
ORGANISM: HERPES VIRUS, TYPE 1
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 CIGGGCTCGGGGTGGGCGGCCGGTCGGTG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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ZIP: 77210
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Conservative
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50.5%;
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                   Score 44; DB 4; Length 4257; Pred. No. 0.16;
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US-08-843-659-1/c
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Best Local (
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APPLICANT: Leopar
APPLICANT: Roizma
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION UNMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:519
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 493
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                                                                                                                                                                    19 CCATCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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ZIP: 77210
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Local Similarity 50.5%;
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                 GGGCCCTCCCGTCCCGCCGGGCGTCGTCGAGGTCGTGGGGGGTCGTCGTGGTCGT
                                                                                                   TAGCGGCCAGCTCGCGCCCTGCCTGGGAAAGCTGTACATGCTGATCGGCGGCGTCGGTGC 138
                                                                                                                                     CCAGCTGTCGCGGCGAGACGGCGTCCCCGGCGTCCTCGCCGGCGTCGCTGCCGCCGCGG
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 GGTCGTCCCCGCCTCCTCCGTCTCCGCGCCCCACCCGAGGGCCCCCCGCTCGTCGCGGT
                                  CGGCGGCCGGGTCTTCCGCCTGCTCGGCGGTGCCGGTCCGTGCGGCCTTTGGCGTCCGCGG 198
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                                                                                                                                                                                                            107;
                                                                                                                                                                                                                                                                                                                              nucleic acid
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Pred. No. 0.16;
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. UNGANISM: Herpes simplex virus;
STRAIN: Herpes Simplex Virus Ty
US-08-458-568A-11
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US-08-458-568A-11
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Best Local Similarity
Matches 107; Conserv
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Compositions and Methods for Treatment of Herpe TITLE OF INVENTION: Infections NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: DF TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERAFECT 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                6120 GGGCCCTCCCGTCCCGGCCGGCGTCGTCGAGGTCGTGGGGGGTGGTCGGGGTCGTGGTCGG
                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 02-JUN
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Philadelphia
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02-JUNE-1995
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                                                                                                                                                                                                              Score 44; DB 1
Pred. No. 0.18;
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6240 CTGGGCTCGGGGTGGGCGGCCGGTCGGTG

230 6271

CGGCGCGATGAGGGCGCCACCTGGGTGGTG

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US-09-568-102-1
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GRGANISM: Soranglum cellulosum
US-09-335-409-1
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                                                                 SEQ ID NO 1
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Best Local Similarity
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                                                                                  CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                              APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                               APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
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APPLICANT: ZIrkle, ROSS
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
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       LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
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RESULT 14 US-09-568-480-1

Sequence 1, Application US/09568480 Patent No. 6355458 GENERAL INFORMATION:

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Best Local Similarity
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Best Local Similarity 52.9
Matches 96; Conservative
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Patent No. 6355457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
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TYPE: DNA
ORGANISM: Sorangium cellulosum
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                                                              GGCGGCGTGGTGCTGGGCCCGTCGTCGTCGGCGCGCGCTCCCTGGGTTCCATCGAGTC
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Zirkle, Ross
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52.5%;
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Pred. No. 0.24;
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APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-09-568-480-1

8.9%; Score 43.8; DB 4; Length 6875/
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; ORGANISM: Sorangium cellulosum
US-09-568-486-1
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Best Local Similarity
Matches 96; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
63965 CGCGCCTTCGGCGAGCTCGCGCGGCGGCGCGCTCCTTC
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ilarity 52.5%;
Conservative
                                                                                     8.9%;
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Pred. No. 0.24;
0; Mismatches 87;
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                                                                    Score 43.8; DB Pred. No. 0.24; 0; Mismatches
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Search completed: December 26, 2002, 06:11:24 Job time : 396 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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  US-09-548-449-3
492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363474 seqs, 203117208 residues
                                                                                                                                                                                                                                                                                                          Published_Applications_NA: *
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Copyright (c) 1993 - 2002 Compugen Ltd
               /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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                                                                                                                                                                                                                                      cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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39.2	39.4	39.4	39.4	39.4	39.4	39.4	39.6	40.2	40.2	40.2	40.2	41	41.8	43.4	43.4	43.8	44	45.6	Score
8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.0	8.2	8.2		8.2	8.3	8.5	8.8	8.8	8.9	8.9	9.3	% Query Match
1771	3152	3032	2561	2561	2561	550	4446	2481	1428	1428	1428	1665	1360	1305	1131	68750	4257	530	Length
9	10	10	12	12	9	10	10	10	10	10	10	10	10	10	9	9	9	9	BB
US-09-991-496-7	US-09-880-107-3431	US-09-954-043-1	US-10-023-523-48	US-10-023-529-48	US-09-976-740-48	us-09-791-171-63	US-09-815-242-7983	US-09-894-998-35	US-09-921-329-5	US-09-921-330-5	US-09-921-232-5	US-09-815-242-7935	US-09-867-550-1927	US-09-815-242-7730	US-09-712-363-93	US-10-014-717-1	US-09-825-288A-1	US-10-073-353-4	ID
Sequence 7, Appli	Sequence 3431, Ap	Sequence 1, Appli	•	Sequence 48, Appl	Sequence 48, Appl	Sequence 63, Appl	Sequence 7983, Ap	Sequence 35, Appl	Sequence 5, Appli	5	Sequence 5, Appli	Sequence 7935, Ap		Sequence 7730, Ap	Sequence 93, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 4, Appli	Description

000000000000000

ALIGNMENTS

RESULT 1 US-10-073-353-4 Sequence 4, Application US/10073353 Patent No. US20020168658A1 GENERAL INFORMATION: REFERENCE/DOCKET NUMBER: 44921-5007-03-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-739-3000
TELEPAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: US/10/073,353
FILING DATE: 03-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,662
FILING DATE: 1996-12-07
APPLICATION NUMBER: US 08/758,662 (CPA)
FILING DATE: 1999-02-17
APPLICATION NUMBER: US 09/585,437
FILING DATE: 2000-06-02
ATTORNEY_AGENT INFORMATION:
NAME: Michael S. Tuscan
REGISTRATION NUMBER: 43,210
PREFEDENCE OF MINNERS: 43,210 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURRENT APPLICATION DATA: COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette CORRESPONDENCE ADDRESS: Namadev Baskaran
TITLE OF INVENTION: Amplification of Nucleic Acids
NUMBER OF SEQUENCES: 8 APPLICANT: Sherman M. Weissman TYPE: nucleic acid ZIP: 20004 STATE: D.C. COUNTRY: USA CITY: Washington ADDRESSEE: Morgan, Lewis & Bockius STREET: 1111 Pennsylvania Ave., NW

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STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-073-353-4
RESULT 3
US-10-014-717-1
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Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS
FILE REFERENCE: ARCD:317USC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR FILING DATE: 1996-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/825,288A CURRENT FILING DATE: 2001-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/259,821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEOPARDI, ROSARIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4257
TYPE: DNA
ORGANISM: HERPES VIRUS, TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 TCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCCATGGTAG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 54.
                                                                                                                                                                                                                                                                                             19 CCATCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCCCCATGG 78
                                                                                             CGGCGCGCGATGAGGGCGCCACCTGGGTGGTG 230
                                                                                                                                                                      CGGCGGCCGGGTCTTCCGCCTGCTCGGCGGTGCCGTCCGTGCGGCCCTTGGCGTCCGCGG 198
                                                                                                                                                                                                                                 TAGCGGCCAGCTCGCGCCCTGCCTGGGAAAGCTGTACATGCTGATCGGCGGCGTCGGTGC 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGCCCGGGCGGCGGCTCCTGGGCGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCGCGATGAGGCCGCCACCTGGGTGG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCCAGCTCGCCCTGCCTGGGAAAGCTGTACATGCTG-ATCGGCGGCGTCGGTGCCG 140
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                                                                                                                                          6CGGCCCGGGCGGCGGCCCCCGGGGGGAGGCGGCGGTGGCGGCCCGGGGGGGCCGGCGGCG
Application US/10014717
                                                                                                                                                                                                                                                                                                                               Conservative
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54.3%;
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50.5%;
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Pred. No. 0.0049;
0; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                            Score 44; DB 9; Length 4257; Pred. No. 0.021;
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RESULT 4
US-09-712-363-93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 93, Application US/09712363 Patent No. US20020164588A1
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Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. US20020192778A1
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/014,717
CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GOETLACH, JOETN
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
                                                                                                    PRIOR PRIOR
                                                                                                                                                PRIOR
                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2000-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schupp, Thomas APPLICANT: Ligon, James APPLICANT: Molnar, Istva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/335,409 PRIOR FILING DATE: 1999-06-17
                                                                                                                                                                     PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63905 CTCACCGAGCGGCAGGTTCTGCTCTCGCTCGTCGCCCTCGCGCTCGTCCTGACCGCG 63964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 CATGGTAGCGGCCAGCTCGCGCCCTGCCTGGGAAAGCTGTACATGCTGATCGGCGGCGTC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 CTTCACCATCGGCCGCAACTCCTGCGGGATATCCTCCTCCTCCTCCTCCACCGGCACCCC 73
                                                                                                                                             APPLICATION NUMBER: 60/118,206 FILING DATE: 1999-02-01
                   APPLICATION NUMBER: 60/134,092 FILING DATE: 1999-05-14
                                                          APPLICATION NUMBER: 60/134,093 FILING DATE: 1999-05-14
APPLICATION NUMBER: 60/165,124
                                                                                                      FILING DATE: 1999-03-26
                                                                                                                        APPLICATION NUMBER: 60/126,593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGCCGGCCGGGTCTTCCGCCTGCTCGGCGGTGCCGGTCCGGTGCGGCCTTGGCCGTC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGGCGTGGTGCTGGGCCCGTCCGTCGTCGCTCGCTCCTTGGGTTCCATCGAGTC 64084
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Zirkle, Ross
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                                                                                                                                                                                                                                                                                                                                                                                 COMPARATIVE ANALYSIS
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-93
밁
                               ρy
                                                                                                                                                  ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1305)
US-09-815-242-7730
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Best Local 9
                                                                                        Query Match 8.8%;
Best Local Similarity 49.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITAA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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NUMBER OF SEQ ID NOS: 292
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                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                         LENGTH: 1305
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
 630
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OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
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CGCGGAACAGCTGGACATGGCGGCGCGCGCGTGCTGCGCGAGCATCCCGGCGTATACCTGCA 689
                                 CGCGGATCATCTTCACCATCGGCCGCAACTCCTGCGGGGATATCCTCGTCCTCCTCCA 63
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                                                                                                                                                                                                                                                                1305
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Similarity 60.7%;
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Yamamoto, Robert T.
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Trawick, John D.
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Pred. No. 0.022;
                                                                     Score 43.4; DB 10;
Pred. No. 0.022;
0; Mismatches 111;
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1927
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-550-1927
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Best Local :
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                                                                                                             APPLICANT:
                      APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITAR. 011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
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TITLE OF INVENTION: No. U520020082206Alel Polynucleotides from Atherogenic Cells
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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Mehraban, Fuad,
                                                                                                                          Zyskind, Judith W. Wall, Daniel Trawick, John D.
                                                                                           Carr, Grant J.
Yamamoto, Robert T.
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Conley, Pamela
                                                                                                                                                                              Ohlsen, Kari L.
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                                                              of
                                                              Essential
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                                                                Genes
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NAME/KEY: CDS
LOCATION: (1)...(1665)
US-09-815-242-7935
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SEQ ID NO 7935
                                                                         SEQ ID NO 5
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Best Local :
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PRIOR FILING DATE: 1997-07-28
PRIOR APPLICATION NUMBER: 09/118,442
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: 09/677,064
                                                                                                                                                                                                                                                                                      FILE REFERENCE: 0706D4
CURRENT APPLICATION NUMBER: US/09/921,232
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/055,446
PRIOR FILING DATE: 1997-08-11
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                               PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-08-08
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Polypeptides Controlling Phytate TITLE OF INVENTION: Metabolism in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Martino-Catt, Susan J.
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PRIOR FILING DATE: 2000-10-23
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              LENGTH: 1428
TYPE: DNA
ORGANISM: Zea mays
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FEATURE:
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Local Similarity 55.2%;
es 80; Conservation
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                                                                                           FastSEQ
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Pred. No. 0.
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; NAME/KEY: CDS
; LOCATION: (118)...(1176)
US-09-921-330-5
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US-09-921-232-5
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/055,446
PRIOR FILING DATE: 1997-08-11
PRIOR APPLICATION NUMBER: 60/055,526
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 60/053,944
PRIOR APPLICATION NUMBER: 09/07-28
PRIOR FILING DATE: 1997-07-28
PRIOR APPLICATION NUMBER: 09/118,442
PRIOR APPLICATION NUMBER: 09/118,442
PRIOR APPLICATION NUMBER: 09/677,064
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ
SEQ ID NO 5
LENGTH: 1428
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Best Local Similarity 49.3%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                Matches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Martino-Catt, Susan J. APPLICANT: Wang, Hongyu APPLICANT: Beach, Larry R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 0706D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Polypeptides Controlling Phytate TITLE OF INVENTION: Metabolism in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Zea mays
  178
                                                                                                                                                                            298
                                        133 CGGTGCCGGCGGCCGGGTCTTCCGCCTGCTCGGCGTGCCGGTCCGTGCGGCCTTGGCGT 192
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                                                                                                                          73 CCATGGTAGCGGCCAGCTCGCGCCCTGCCTGGGAAAGCTGTACATGCTGATCGGCGGCGT 132
                                                                                                                                                                                                   13 TCTTCACCATCGGCCGCAACTCCTGCGGGATATCCTCGTCCTCCTCCTCCACCGGCACCC 72
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                                                                                                                                                                       TCCTGGCGAGCCCCCGGAGCTTGGGCTGGAGGAAGCTCTTGGCCTTCTTCGTCGTGAGCG 239
CCGGAGGCGCCGCCGCGCGCCCCCCCCCCCCCCCCCCACGCACCCCACGCACACACACA 119
                                                                                 CGTACCCCACCACCACCTCCCGCGCGCGGGAGGCGCCGCCACCACCGGCTCCTCCGCGGCCT
                                                                                                                                                                                                                                                                Conservative
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49.3%;
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; LOCATION: (118)...(1176)
US-09-921-329-5
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CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/055,446
PRIOR FILING DATE: 1997-08-11
PRIOR APPLICATION NUMBER: 60/055,526
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 60/053,944
PRIOR FILING DATE: 1997-07-28
PRIOR FILING DATE: 1997-07-28
PRIOR FILING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-17
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APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
                                                   APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Polypeptides Controlling Phytate TITLE OF INVENTION: Metabolism in Plants FILE REFERENCE: 0706D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Martino-Catt, Susan
APPLICANT: Wang, Hongyu
APPLICANT: Beach, Larry R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/677,064
PRIOR FILING DATE: 2000-09-29
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGAGGCGCCGCCGCGCGCCTCCCCCCCCCCCCCACGCACCCCGCCAGACACCA 119
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49.3%;
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; LENGTH: 2481
; TYPE: DNA
; ORGANISM: HSV-2
US-09-894-998-35
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US-09-815-242-7983/c
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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Best Local Similarity
Matches 93; Conserv
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                                                                                                      SOFTWARE: Fas
SEQ ID NO 7983
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CURRENT APPLICATION NUMBER: US/09/894,998
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                            PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                           NUMBER OF SEQ ID NOS:
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NAME/KEY:
                                          LENGTH: 4446
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                   FEATURE:
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                                                                                                                         FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Danie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick, John D.
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                                                                                                                         4.0
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LENGTH: 550
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-791-171-63
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US-09-791-171-63/c
; Sequence 63, App
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CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
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Best Local S
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TITLE OF INVENTION: UDCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERLYED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/070,488 PRIOR FILING DATE: 1998-01-05
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Local Similarity 50.3%;
les 97; Conservative
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                                                                 ACTGCTCCTCGGCAGCCTCGACGGCGCACCGGCCGGGGGGGCGCACCGGCGGCGACGG
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CGACTGGAGCGGCGGCGGTGACCTCGAAGGTCTCCTCGAACTTCTTGACGAAGTCGGAGA
                                  CTGCTGCTTGGCGGTCTCGCCGGGGAGGATCTCCAGCAGGTCGGTGCGGCCGATCAGCTC 3478
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Similarity 49.5%;
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RASMUSSEN, Peter Birk
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US-09-976-740-48
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SOFTWARE: Fasts
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FENGTH: 2561
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PRIOR FILING DATE: 2000-07-14
PRIOR PPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Lees, Ann M.
                                                                                                                                                                                                                                Sequence 48, Application US/10023529 Patent No. US20020129388A1
APPLICANT: LAW, SIMON W.
APPLICANT: ARJONA, ANIBAL A.
APPLICANT: ARJONA, ANIBAL A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
CURRENT FILING DATE: 2001-12-17
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Best Local Similarity
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Publication No.
                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: APROTEINS AND THEIR USE IN DIAGNOSING TITLE OF INVENTION: APROFENSIS
FILE REFERENCE: 10797-004001
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Law, Simon W.
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Pred. No. 0.28;
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 06/031,330
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ 1D NOS: 53
SOSTWARE: FEASTER
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ 1D NOS: 53
SOSTWARE: FEASTER
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
SOSTWARE: FEASTER
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ 10 NOS: 53
SOSTWARE: PASTER
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ 10 NOS: 53
SOSTWARE: PASTER
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ 10 NOS: 53
SOSTWARE: PASTER
PRIOR PILING DATE: 1997-06-03
NUMBER: US 60/048,547
NUMBER: US 60/04
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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	Human secreted pro Candida albicans-s Oligonucleotide SE	Staphylococcus aur 3'-5' micF RNA str	Tetracycline promo HBV infection regu		Human SNP oligonuc Leucine zipper-hum			> >	PABF	prin	tpiA gene PCR prim	al-time vali	Cyclin Bi ribozyme Forward PCR primer	B1		Oligonucleotide SE	ß	igonucleotide	Oligonucleotide SE

ALIGNMENTS

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13-APR-2000; 2000US-0548449
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Dolan J, Pan W;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; infection; drug-resistant pathogen; cancer; typhoid fever; bacterial meningitis; tuberculosis; antisense strand; ribozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2001 (first entry)
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                                                                                                                                                                                                                                    (MUSC-) MUSC FOUND RES DEV. (UYPE-) UNIV PENN STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxic protein; ds.
                                                                                                                                   Clawson G,
                                                                                                                                            'n
                                                                                                                                        Schofield D,
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RESULT 2
ABA02585
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        The invention relates to the discovery, identification and method characterisation of toxic agents lethal to pathogens and method targeting such toxic agents to a pathogen or pathogen infected order to treat and/or eradicate the infection. In particular the invention relates to at least one nucleic acid molecule, which specifically hybridises to mRNA encoding at least one vital prospectifically hybridises to mRNA encoding at least one vital prospectifically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence comprises the consensus IHF binding site, wh was used in the construction of the pathogen and tissue-specific agents of the invention. These agents may be antisense sequences ribozymes or toxic proteins. These can be used in the treatment o and infections including hepatitis, herpes, malaria, bacterial
 associated
                                                                                               Examples;
                                                                                                                    Novel nucleic acid for the treatment of papilloma or induced conditions comprises a catalytic region which cytotoxic or cytostatic effect in the infected cell -
                                                                                                                                                                                            Norris
Hoel B,
                                                                                                                                                                                                                                                                      07-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA02585-standard; DNA, L3 BP.
                                                                                                                                                                                                                                                                                13-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                     cervical dys
                                                                                                                                                                                                                                                                                                                                                                                                                                         Infection; antisense RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IHF binding site consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÆBA02585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          meningitis, typhoid fever and tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid comprising a nucleotide sequence encoding one or more toxic agents operably linked to a pathogen specific or tissue specific promoter is useful for inhibiting replication of a
                                                                                                                                                                                                                                                                                                                                                                                                                              papilloma virus;
                                                                                                                                                                                                                                 PENN-)
                                                                                                                                                                                                                                              UYSC-)
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                                                                                                                                                                                                                                                                                                                                                                                                      dysplasia;
ing site; s
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                                                                                             Page
                                                                                                                                                                                              Dolan
 with
                                                                                                                                                                                                        Clawson
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STATE
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2000US-251810P.
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RES FOUND
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 transformation or
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s B virus; gytotoxic; cytostatic; wart;
                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
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Pred. No.
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produces a
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

specification, but was obtained in electration.int/pub/published_pct_sequences

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

Claim methylation

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IJ.

22997;

29pp +

Sequence Listing;

German

Set of oligonucleotides,

useful for diagnosis and cell typing, a nucleotide polymorphisms and cytosine

S

designed to

status detect single WPI; 01ek

2001-657177/75.

Piepenbrock C,

Berlin

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07-APR-2000; 2000DE-1019173 06-APR-2001; 2001WO-IB00713

18-OCT-2001

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Best Local
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ABC22980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human;
peptide nucleic acid; cytosine methylation;
central nervous system; gastrointestinal; re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200177384-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide
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system; gastrointestinal; respiratory; immune; metal
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cardiovascular; primer;
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the invention re
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RESULT 5
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                                                                                               Matches
                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA.) The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01ek
                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single nucleotide polymorphisms and cytosine methylation status
                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 22998; 29pp +
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                                                                       AATCAANNANTTA 13
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                                                                                                                                                BP; 7
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                                                                                                Conservative
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                                                                                                                                               A; 2 C; 0 G; 4 T; 0 other;
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Pred. No.
                                                                                             Score 10; DB 23;
Pred. No. 1.1e+04
0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Sequence Listing; German.
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Mismatches 3
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RESULT 6
ABC22931
ID ABC2
XX
AC ABC2
XX
AC ABC2
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DT 20-F
XX
DE 0119
XX
KW SNP;
KW SNP;
KW Pept
KW pept
KW cent
XX
OS Homo
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Best Local
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                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                      Oligonucleotide
                                                                                                                                                                             ABC22983 standard;
                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 BP; 3 A; 0 C; 2 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 22999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-APR-2000; 2000DE-1019173
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central nervous
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                                                                                                                   20-FEB-2002
                                                                                                                                                ABC22983;
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                 (first
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ABF44524/c
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                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; peptide nucleic acid; cytosine methylation; cardiovascular; primer; central nervous system; gastrointestinal; respiratory; immune; meta
                                                                                                                                                                                                                                                                                                                                                                                                                                                     and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory.
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         Olek A,
                                               07-APR-2000; 2000DE-1019173
                                                                06-APR-2001; 2001WO-IB00713
                                                                                     18-OCT-2001.
                                                                                                                                                                                                                                          ABF44524 standard;
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 23000;
                                                                                                                                                                                  Oligonucleotide SEQ
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                                                                                                                                                                                                                        ABF44524;
                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 8 A; 2 C; 0 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
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         Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         onucleotides, useful for diagnosis and cell typing, detect single nucleotide polymorphisms and cytosin
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                 ID NO 144521 for detecting
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76.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel oligonucleotide
         Berlin
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                                                                                                                                                                                 SNP TSC0036340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primers or peptide nucleic
eotide polymorphisms (SNP)
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                                                                                                                                                                                                                                                                                                                                              Length 13;
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                                                                                                                                                              cancer;
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                                                                                                                                             metabolic
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                                                                                    Query Match
Best Local
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      designed to detect single nucleotide polymorphisms and cytosine methylation status - \,
                                                                                                                                                                      oligomers are also used for detecting cell type differentiation.
ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
ABI000110-ABH82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
                                                                                                                                        Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   This invention descri
acid (PNA) oligomers
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 144521; 29pp + Sequence Listing;
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                  1 AATCAANNANTTA 13
AATCAATAAATTA
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                                                                      10;
                                                                                      Similarity
                                                                      Conservative
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                                                                                    76.98;
76.98;
                                                                    0,
                                                                                    Score 10;
Pred. No.
                                                                    Mismatches
                                                                                   1.1e+04;
                                                                                                     DB 23;
                                                                                                     Length 13
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                                                                    Indels
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RESULT 8
ABF44525
                                                            SNP; single nucleotide polymorphism; human;
peptide nucleic acid; cytosine methylation;
central nervous system; gastrointestinal; re
                                                                                                                             Oligonucleotide
WO200177384-A2
                             Homo sapiens
                                                                                                                                                              21-FEB-2002
                                                                                                                                                                                               ABF44525;
                                                                                                                                                                                                                              ABF44525 standard;
                                                                                                                                                             (first entry)
                                                                                                                             SEQ
                                                                                                                                                                                                                                DNA;
                                                                                                                             ID NO 144522 for
                                                                                                                                                                                                                                13
                                                                                                                            detecting
                                                            n; diagnosis; PNA; cancer;
n; cardiovascular; primer;
respiratory; immune; metak
                                                                                                                             SNP TSC0036340
                                                                        CNS;
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07-APR-2000; 2000DE-1019173

06-APR-2001; 2001WO-IB00713

18-OCT-2001.

01ek

P

Berlin

7

(EPIG-)

EPIGENOMICS Piepenbrock C,

ĄG

WPI;

2001-657177/75

Set of oligonucleotides,

useful

nucleotide

diagnosis and polymorphisms

cell typing, s s and cytosine

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Claim 1; SEQ ID 144522; designed to detect single methylation status

29pp +

Sequence Listing; German.

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RESULT 9
ABF44556/c
ID ABF445
XX ABF445
XX ABF445
XX SNP; g
COLigon
XX SNP; g
KW Peptid
KW Centra
XX Homo s
YX Centra
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YX Set oi
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Best Local S
Matches 10
                                                                                                                                                                                                                     and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF89989, ABF00010-ABF89989 and ABI00010-ABF89989, ABF00010-ABF89989, ABF900010-ABF89989, ABF900010-ABF89989, ABF900010-ABF89989, ABF900010-ABF89989, ABF900010-ABF89989, ABF900010-ABF99989, ABF900010-ABF99999, ABF900010-AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      designed to detect single nucleotide polymorphisms and methylation status -
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ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABH00010-ABH82073 represent the oligomers described in the invention.
NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATCAANNANTTA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes novel oligonucleotide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                                                           SEQ
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                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                      ID NO 260430 for detecting SNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
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                                                                                                                                                                                                                                                                                 entry)
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76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e polymorphism; human; diagnosis; PNA;
cytosine methylation; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                             13
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Pred. No. 1.1e+04;
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ular; primer;
immune; metab
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cimer; ss;
metabolic.
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RESULT 13
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid (PNA) oligomers for detecting single nucleotide primers or peptide nucleic acid (YNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for disgnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                                                                                                                                                          Oligonucleotide SEQ ID NO 260431 for detecting SNP TSC0063245
                                                                                                                                                                                                                                                                                                                                                                                   ABH60454;
                                                                                                                                                                                                                                                                                                                                                                                                              ABH60454 standard;
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                                                                                                                                                                                                                    WO200177384-A2
                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek
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                                                                                                                                                                                                                                              sapiens.
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detect single nucleotide status -
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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76.98;
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Pred. No.
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single $\cdot nucleotide$ polymorphisms and cytosine methylation status -

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Piepenbrock C,

Berlin K;

2001-657177/75

(EPIG-)

EPIGENOMICS

ΑG

07-APR-2000; 2000DE-1019173

06-APR-2001; 2001WO-IB00713

18-OCT-2001

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RESULT 14
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation.

ABCO0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABF00010-ABF8073 represent the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed
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ABC00010-ABC99989, ABP00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABE39989, are present the oligomers described in the invention.

NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide n acid (PNA) oligomers for detecting single nucleotide polymorphisms and cytosine methylation status in chemically pretreated genomic DN oligonucleotides are used for diagnosis and/or prognosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligonucleotides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detect single nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                              ID 260432;
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76.98;
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Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 T;
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     The present invention describes enzymatic nucleic acid molecules with CR NAA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARWT) gene, an integrin subunit beta 3 creater an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA1675 to AAA17167 to AAA17561 to AAA1762 represent ribozyme sequences for ARWT, and AAA17168 to AAA17560 and AAA17623 to AAA17864 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19123 to AAA19222 represent their corresponding target sequences; AAA19123 to AAA19222 represent their corresponding target sequences; AAA19125 to AAA19222 represent their corresponding target sequences; AAA19125 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA22475 and AAA3263 to AAA23363 to AAA23363 to AAA2342 represent ribozyme sequence for integrin subunit beta 3, and AAA2376 to AAA2362, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or integrin subunit heta 3 integrin subunit alpha 6 corresponding target sequences. The ribozymes of integrin subunit heta 3 integrine subunit father 6 corresponding target sequences.
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ftp.wipo.int/pub/published_pct_sequences.
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BH854706 SALK_0889
AZ439152 1M0229G08
BH854728 SALK_0889
                                                                                                                      Description
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ALIGNMENTS

AU258344 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0012727 3', mRNA sequence.

ACCESSION AU258344
VERSION AU258344 GI:20323820

KEYMORDS SOURCE ONGANISM BUSCULUS CDNA clone

Mus musculus

Mus musculus

FERENCE 1 (bases 1 to 21)

AUTHORS Kato, K. and Matoba, R.

TITLE Generation of expressed sequence tags from mouse brain
Unpublished (2002)
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences

Mara Institute of Science and Technology

By 16-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581
Fax: 81-743-72-5581
Fax: 81-743-72-5581
Fax: 81-743-72-5581
Location/Qualifiers

Source /organism="Mus musculus"
//bb_xref="taxon:10090"
//clone="BED0012727"

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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
BH854703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is single pass sequence recovered from the left border TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zinmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ecker@salk.edu
                                                                                                                                                                                                                                                                  /clone="SALK_088982.46.95.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCIR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used or
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/tissue_type="brain"
/note="Vector: pGEM-T-easy"
2 c 1 g 7 t
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                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3702"
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Insert Length: 10000 Std Error: (
Insert Length: Tow: M column: 13
Plate: 0132 row: M column: 13
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Tel: 801 585 5606
Fax: 801 585 7177
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Contact: Robert B.
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Eukaryota; Metazoa;
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                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
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76.9%;
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Score 10; DB pred. No. 4.2e 0; Mismatches
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                                              DB 17;
4.2e+04;
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RESULT 5
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      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                          Mus musculus
                                                                                                                                                                                       GSS.
                                                                                                                                                                                                                            AZ439152
                                                                                                                                                                                                                                             1M0229G08R Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0229G08 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis Genome Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH854706 34 bp DNA linear GSS 08-JUL-2002 SALK_088979.46.35.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_088979.46.35.x, DNA
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                                                                                                                                                                                                                                                                                        AZ439152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is single pass sequence recovered from the left border TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   At5g53910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Sequence-Indexed Library of Insertion Mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alonso, J.M., Leisse, T.J., Barajas, P.,
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                                                                             mmalia; Eutheria; (bases 1 to 35)
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Wright, D., Weiss, R.
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/dlone="SALK_088979.46.35.x"
/clone="Farabidopsis thaliana TDNA insertion lines"
/clone="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 3 c 4 g 15 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/strain="Columbia 0"
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76.9%;
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Pred. No. 4.3e+04;
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                                                                                                                                                                                                                                                                musculus
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RESULT 6
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                                                                                                                                                                                                                       AATCAATCATTTA 18
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вн854728
вн854728.1
                                          sequence.
                                                          BH854728 36 bp DNA linear GSS SALK_088935.40.95.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_088935.40.95.x,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (g1|4732114 gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                        purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0229G08"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
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/strain="C57BL/6J"
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76.9%;
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Genome Center
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rches 3;
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                                                                                                                                                                                                                                                                                                              Gaps
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Alonso, J.M., Leisse, T.J.,

Barajas, P., Chen, H., Kim, C.J., Parker, H.,

Cheuk, R., G Prednis, L.,

Gadrinab

Jeske,A.,

(bases

1 to 36)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Arabidopsis thaliana

thale cress

GSS

GI:21704318

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REFERENCE
AUTHORS
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                                                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                          Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                 Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                        ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L
, Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH854701 37 bp DNA linear GSS SALK_088987.31.80.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_088987.31.80.x,
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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                                         At5g53910
                                                                                                                                                                                                                                          Contact: Joseph R. Ecker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,F. Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/note="PCR was performed on Arabidopsis thallana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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               directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" 3 c 7 g 15 t
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/note-"PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
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/strain="Columbia 0"
/db_xref="taxon:3702"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reill,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: A column: 08
Seg primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                             þ
                                                                                                                                                              10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (g1[4732114]sp[hgF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                           http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                   adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."

3 5 c 7 g 25 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0102A08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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0; Mismatches 3;
     Score 10;
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DB 17;
  Length 46;
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AZ508716/c
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ORIGIN
                       BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Time 1 1000 Std Std Erro
Time 1 1000 Std Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ508716 46 bp D
IM0351114F Mouse 10kb plasmid UUGC1M
Clone UUGC1M0351114 F, DNA sequence.
AZ508716
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Location/Qualifiers
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Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ508716.1 GI:10690032
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       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
                       17
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                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0351I14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, .F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
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0; Mismatches 3;
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Query Match

76.98;

Score 10;

DB 17;

Length 46;

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BASE COUNT
ORIGIN
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AZ481968/c
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   Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B. We
University of Utah Ge
University of Utah
Rm. 308, Biomedical F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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100306110R Mouse 10kb plasmid UUGC1M library Clone UUGC1M0306110 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0306 row: I column: 10
Seg primer: CACACAGGAAACAGCTATGACC
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Mammalia; Eutheria; Rodentia;
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801 585 7177
                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: PWD42nv; Purified genomic musculus C57BL/6J (male) was obtained fr
                                                                                                                                                                                                                                                                                                                                                                          Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="UUGC1M0306I10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
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 76.98;
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0; Mismatches 3;
Score 10;
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                            ,C., Jeske,A., Karnes,M.,
Zimmerman,J. and Ecker,J.
A Sequence-Indexed Library
Arabidopsis Genome
                                                                                                              SALK_049225 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_049225, DNA sequence. BH810378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Nori Satch
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Unpublished (2001)
Contact: Joseph R.
                                                                               Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H.,
Alonso,J.M., Leisse,T.J., Kim,C.J., Parker,H.,
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Expressed genes in Ciona intestinalis
Unpublished (2000)
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Phlebobranchia; Cionidae; Ciona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     satoh@ascidian.zool.kyoto-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Nori Satoh unpublished cDNA library, larva"
/tissue_type="whole animal"
/dev_stage="larva"
/note="Vector: pBluescript SK"
9 c 3 g 20 t
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/db_xref="taxon:7719"
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., G., C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Zimmerman,J. and Ecker,J.R.
A Sequence Indexed Library of Insertion Mutations in the
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/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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/strain="Columbia 0"
                                                                      /strain="Columbia 0"
/db_xref="taxon:3702"
                                                                                                                                                                Location/Qualifiers
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/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
                                                  /clone="SALK_081694"
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/strain="Columbia 0"
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AATCAAGGACTTA
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10; Conserv
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10; Conser
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BED0010699 3', mRNA sequence.
                                                                                                                                                                                                                                                                                         Contact: Kikuya Kato Graduate School of Biological Sciences Nara Institute of Science and Technology 8916-5 Takayama, Ikoma, Nara 630-0101, Jt Tel: 81-743-72-5581
                                                                                                                                                                                                                                               Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
                                                                                                                                                                                                                                                                                                                                                              Generation of expressed sequence tags from mouse brain Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                        Kato, K. and Matoba, R.
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
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                                                                                                                      /clone_lib="3'-directed mouse
/tissue_type="brain"
/note="Vector: pgeM-T-easy"
9 c 7 g 17 t
                                                                                                                                                                             /db_xref="taxon:10090"
/clone="BED0010699"
                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                   ocation/Qualifiers
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cDNA library Mus
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5e+04;
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